Patin Docket Preview

Sequence Listing

<110> Chen, Jian
Goddard, Audrey
Gurney, Austin L.
Hillan, Kenneth
Pennica, Diane
Wood, William I.
Yuan, Jean

<120> Secreted and Transmembrane Polypeptides and Nucleic Acids Encoding the Same

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<130> P1618P2C3

<140> US 09/903,806
<141> 2001-07-11

<150> US 09/665,350
<151> 2000-09-18

<150> PCT/US00/04414
<151> 2000-02-22

<150> PCT/US98/18824
<151> 1998-09-10

<150> US 60/062,287
<151> 1997-10-17

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cgccgggccg cgctggggct cctgccgctt ctgctgctgc tgccgcccgc 200

gccggaggcc gccaagaagc cgacgccctg ccaccggtgc cgggggctgg 250

tggacaagtt taaccagggg atggtggaca ccgcaaagaa gaactttggc 300

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gaagacactg aaagtgtgct gctctccagg aacctacggt cccgactgtc 550

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aacgaaaact gctacaatac tccagggagc tacgtctgtg tgtgtcctga 1100

cggcttcgaa gaaacggaag atgcctgtgt gccgccggca gaggctgaag 1150

ccacagaagg agaaagcccg acacagctgc cctcccgcga agacctgtaa 1200

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gcctgctctc taacggttga ttctcatttg tcccttaaac agctgcattt 1350

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<212> PRT
<213> Homo Sapien

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Cys His Arg Cys Arg Gly Leu Val Asp Lys Phe Asn Gln Gly Met
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Val Asp Thr Ala Lys Lys Asn Phe Gly Gly Gly Asn Thr Ala Trp
                  50                  55                  60

Glu Glu Lys Thr Leu Ser Lys Tyr Glu Ser Ser Glu Ile Arg Leu
                  65                  70                  75

Leu Glu Ile Leu Glu Gly Leu Cys Glu Ser Ser Asp Phe Glu Cys
                  80                  85                  90

Asn Gln Met Leu Glu Ala Gln Glu Glu His Leu Glu Ala Trp Trp
                  95                 100                 105

Leu Gln Leu Lys Ser Glu Tyr Pro Asp Leu Phe Glu Trp Phe Cys
                 110                 115                 120

Val Lys Thr Leu Lys Val Cys Cys Ser Pro Gly Thr Tyr Gly Pro
                 125                 130                 135

Asp Cys Leu Ala Cys Gln Gly Gly Ser Gln Arg Pro Cys Ser Gly
                 140                 145                 150

Asn Gly His Cys Ser Gly Asp Gly Ser Arg Gln Gly Asp Gly Ser
                 155                 160                 165

Cys Arg Cys His Met Gly Tyr Gln Gly Pro Leu Cys Thr Asp Cys
                 170                 175                 180

Met Asp Gly Tyr Phe Ser Ser Leu Arg Asn Glu Thr His Ser Ile
                 185                 190                 195

Cys Thr Ala Cys Asp Glu Ser Cys Lys Thr Cys Ser Gly Leu Thr
                 200                 205                 210

Asn Arg Asp Cys Gly Glu Cys Glu Val Gly Trp Val Leu Asp Glu
                 215                 220                 225

Gly Ala Cys Val Asp Val Asp Glu Cys Ala Ala Glu Pro Pro Pro
                 230                 235                 240

Cys Ser Ala Ala Gln Phe Cys Lys Asn Ala Asn Gly Ser Tyr Thr
                 245                 250                 255

Cys Glu Glu Cys Asp Ser Ser Cys Val Gly Cys Thr Gly Glu Gly
                 260                 265                 270

Pro Gly Asn Cys Lys Glu Cys Ile Ser Gly Tyr Ala Arg Glu His
                 275                 280                 285

Gly Gln Cys Ala Asp Val Asp Glu Cys Ser Leu Ala Glu Lys Thr
                 290                 295                 300

Cys Val Arg Lys Asn Glu Asn Cys Tyr Asn Thr Pro Gly Ser Tyr
                 305                 310                 315

Val Cys Val Cys Pro Asp Gly Phe Glu Glu Thr Glu Asp Ala Cys
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cgcccagccg tctaaacggg aacagccctg gctgagggag ctgcagcgca 150

gcagagtatc tgacggcgcc aggttgcgta ggtgcggcac gaggagtttt 200

cccggcagcg aggaggtcct gagcagcatg gcccggagga gcgccttccc 250

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gggcggaggc cgggccgccg caggaggaga gcctgtacct atggatcgat 350

gctcaccagg caagagtact cataggattt gaagaagata tcctgattgt 400

ttcagagggg aaaatggcac cttttacaca tgatttcaga aaagcgcaac 450

agagaatgcc agctattcct gtcaatatcc attccatgaa ttttacctgg 500

caagctgcag ggcaggcaga atacttctat gaattcctgt ccttgcgctc 550

cctggataaa ggcatcatgg cagatccaac cgtcaatgtc cctctgctgg 600

gaacagtgcc tcacaaggca tcagttgttc aagttggttt cccatgtctt 650

ggaaaacagg atggggtggc agcatttgaa gtggatgtga ttgttatgaa 700

ttctgaaggc aacaccattc tccaaacacc tcaaaatgct atcttcttta 750

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ctgtgagaaa gccctttgta ccccacgatg tatgaatggt ggactttgtg 900

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ccctggaaaa tgtatttgcc ctccaggact agagggagag cagtgtgaaa 1050

tcagcaaatg cccacaaccc tgtcgaaatg gaggtaaatg cattggtaaa 1100

agcaaatgta agtgttccaa aggttaccag ggagacctct gttcaaagcc 1150

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aatgccaatg tcaagaaggt tggcatggaa gacactgcaa taaaaggtac 1250

gaagccagcc tcatacatgc cctgaggcca gcaggcgccc agctcaggca 1300

gcacacgcct tcacttaaaa aggccgagga gcggcgggat ccacctgaat 1350

ccaattacat ctggtgaact ccgacatctg aaacgtttta agttacacca 1400

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gaaataggga atataatgta tgaacttttt gcattggctt gaagcaatat 2000

aatatattgt aaacaaaaca cagctcttac ctaataaaca ttttatactg 2050

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<211> 379
<212> PRT
<213> Homo Sapien

<400> 4

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Pro Gln Glu Glu Ser Leu Tyr Leu Trp Ile Asp Ala His Gln Ala
35 40 45

Arg Val Leu Ile Gly Phe Glu Glu Asp Ile Leu Ile Val Ser Glu
50 55 60

Gly Lys Met Ala Pro Phe Thr His Asp Phe Arg Lys Ala Gln Gln
65 70 75

Arg Met Pro Ala Ile Pro Val Asn Ile His Ser Met Asn Phe Thr
80 85 90

Trp Gln Ala Ala Gly Gln Ala Glu Tyr Phe Tyr Glu Phe Leu Ser

95 100 105

Leu Arg Ser Leu Asp Lys Gly Ile Met Ala Asp Pro Thr Val Asn
110 115 120

Val Pro Leu Leu Gly Thr Val Pro His Lys Ala Ser Val Val Gln
125 130 135

Val Gly Phe Pro Cys Leu Gly Lys Gln Asp Gly Val Ala Ala Phe
140 145 150

Glu Val Asp Val Ile Val Met Asn Ser Glu Gly Asn Thr Ile Leu
155 160 165

Gln Thr Pro Gln Asn Ala Ile Phe Phe Lys Thr Cys Gln Gln Ala
170 175 180

Glu Cys Pro Gly Gly Cys Arg Asn Gly Gly Phe Cys Asn Glu Arg
185 190 195

Arg Ile Cys Glu Cys Pro Asp Gly Phe His Gly Pro His Cys Glu
200 205 210

Lys Ala Leu Cys Thr Pro Arg Cys Met Asn Gly Gly Leu Cys Val
215 220 225

Thr Pro Gly Phe Cys Ile Cys Pro Pro Gly Phe Tyr Gly Val Asn
230 235 240

Cys Asp Lys Ala Asn Cys Ser Thr Thr Cys Phe Asn Gly Gly Thr
245 250 255

Cys Phe Tyr Pro Gly Lys Cys Ile Cys Pro Pro Gly Leu Glu Gly
260 265 270

Glu Gln Cys Glu Ile Ser Lys Cys Pro Gln Pro Cys Arg Asn Gly
275 280 285

Gly Lys Cys Ile Gly Lys Ser Lys Cys Lys Cys Ser Lys Gly Tyr
290 295 300

Gln Gly Asp Leu Cys Ser Lys Pro Val Cys Glu Pro Gly Cys Gly
305 310 315

Ala His Gly Thr Cys His Glu Pro Asn Lys Cys Gln Cys Gln Glu
320 325 330

Gly Trp His Gly Arg His Cys Asn Lys Arg Tyr Glu Ala Ser Leu
335 340 345

Ile His Ala Leu Arg Pro Ala Gly Ala Gln Leu Arg Gln His Thr
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365 370 375

Asn Tyr Ile Trp

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<400> 9
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<210> 10
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<210> 11

<211> 2197
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<213> Homo Sapien

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<213> Homo Sapien

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Leu Ala Pro Gly Leu His Leu Arg Gly Ile Arg Asp Ala Gly Gly
             35                  40                  45

Arg Tyr Cys Gln Glu Gln Asp Leu Cys Cys Arg Gly Arg Ala Asp
             50                  55                  60

Asp Cys Ala Leu Pro Tyr Leu Gly Ala Ile Cys Tyr Cys Asp Leu
             65                  70                  75

Phe Cys Asn Arg Thr Val Ser Asp Cys Cys Pro Asp Phe Trp Asp
             80                  85                  90

Phe Cys Leu Gly Val Pro Pro Pro Phe Pro Pro Ile Gln Gly Cys
             95                 100                 105

Met His Gly Gly Arg Ile Tyr Pro Val Leu Gly Thr Tyr Trp Asp
            110                 115                 120

Asn Cys Asn Arg Cys Thr Cys Gln Glu Asn Arg Gln Trp His Gly
            125                 130                 135
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Ala Gly Trp Glu Pro Gln Arg Leu Leu Gly His Asp Pro Gly
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<212> DNA
<213> Homo Sapien

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<223> unknown base

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gaacctgctg tcttgtacac ccaccagcag cagggctgcc gcgntgggcg 150

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<400> 15
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<210> 16
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<212> DNA
<213> Artificial Sequence

<220>
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<210> 17
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<212> DNA
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cgcagttggc ctcctgaccg tcatcagcaa aggctgcagc ttgaactgcg 200

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35 40 45

Ser Gly Asp Pro Ala Ser Tyr Arg Leu Trp Gly Ala Pro Leu Gln
50 55 60

Pro Thr Leu Gly Val Val Pro Gln Ala Ser Val Pro Leu Leu Thr
65 70 75

Asp Leu Ala Gln Trp Glu Pro Val Leu Val Pro Glu Ala His Pro
80 85 90

Asn Ala Ser Leu Thr Met Tyr Val Cys Thr Pro Val Pro His Pro
95 100 105

Asp Pro Pro Met Ala Leu Ser Arg Thr Pro Thr Arg Gln Ile Ser
110 115 120

Ser Ser Asp Thr Asp Pro Pro Ala Asp Gly Pro Ser Asn Pro Leu
125 130 135

Cys Cys Cys Phe His Gly Pro Ala Phe Ser Thr Leu Asn Pro Val
140 145 150

Leu Arg His Leu Phe Pro Gln Glu Ala Phe Pro Ala His Pro Ile
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Tyr Asp Leu Ser Gln Val Trp Ser Val Val Ser Pro Ala Pro Ser
170 175 180

Arg Gly Gln Ala Leu Arg Arg Ala Gln
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<210> 19
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<220>
<223> Synthetic Oligonucleotide Probe

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<210> 20
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 20
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<212> DNA
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<220>
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<211> 1200
<212> DNA
<213> Homo Sapien

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gtgagggacc agggcgccat gaccgaccag ctgagcaggc ggcagatccg 150

cgagtaccaa ctctacagca ggaccagtgg caagcacgtg caggtcaccg 200

ggcgtcgcat ctccgccacc gccgaggacg gcaacaagtt tgccaagctc 250

atagtggaga cggacacgtt tggcagccgg gttcgcatca aaggggctga 300

gagtgagaag tacatctgta tgaacaagag gggcaagctc atcgggaagc 350

ccagcgggaa gagcaaagac tgcgtgttca cggagatcgt gctggagaac 400

aactatacgg ccttccagaa cgcccggcac gagggctggt tcatggcctt 450

cacgcggcag gggcggcccc gccaggcttc ccgcagccgc cagaaccagc 500

gcgaggccca cttcatcaag cgcctctacc aaggccagct gcccttcccc 550

aaccacgccg agaagcagaa gcagttcgag tttgtgggct ccgcccccac 600

ccgccggacc aagcgcacac ggcggcccca gcccctcacg tagtctggga 650

ggcagggggc agcagcccct gggccgcctc cccacccctt tcccttctta 700

atccaaggac tgggctgggg tggcgggagg ggagccagat ccccgaggga 750

ggaccctgag ggccgcgaag catccgagcc cccagctggg aaggggcagg 800

ccggtgcccc aggggcggct ggcacagtgc ccccttcccg gacgggtggc 850

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tgccggcctc ccagccgggc tcctgaagcc cgctgaaagg tcagcgactg 950

aaggccttgc agacaaccgt ctggaggtgg ctgtcctcaa aatctgcttc 1000

tcggatctcc ctcagtctgc ccccagcccc caaactcctc ctggctagac 1050

tgtaggaagg gacttttgtt tgtttgtttg tttcaggaaa aaagaaaggg 1100

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cctgcacccc acccccaact cccagccccg gaataaaacc attttcctgc 1200

<210> 23
<211> 205

<212> PRT
<213> Homo Sapien

<400> 23
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1 5 10 15

Leu Leu Ile Leu Cys Cys Gln Thr Gln Tyr Val Arg Asp Gln Gly
20 25 30

Ala Met Thr Asp Gln Leu Ser Arg Arg Gln Ile Arg Glu Tyr Gln
35 40 45

Leu Tyr Ser Arg Thr Ser Gly Lys His Val Gln Val Thr Gly Arg
50 55 60

Arg Ile Ser Ala Thr Ala Glu Asp Gly Asn Lys Phe Ala Lys Leu
65 70 75

Ile Val Glu Thr Asp Thr Phe Gly Ser Arg Val Arg Ile Lys Gly
80 85 90

Ala Glu Ser Glu Lys Tyr Ile Cys Met Asn Lys Arg Gly Lys Leu
95 100 105

Ile Gly Lys Pro Ser Gly Lys Ser Lys Asp Cys Val Phe Thr Glu
110 115 120

Ile Val Leu Glu Asn Asn Tyr Thr Ala Phe Gln Asn Ala Arg His
125 130 135

Glu Gly Trp Phe Met Ala Phe Thr Arg Gln Gly Arg Pro Arg Gln
140 145 150

Ala Ser Arg Ser Arg Gln Asn Gln Arg Glu Ala His Phe Ile Lys
155 160 165

Arg Leu Tyr Gln Gly Gln Leu Pro Phe Pro Asn His Ala Glu Lys
170 175 180

Gln Lys Gln Phe Glu Phe Val Gly Ser Ala Pro Thr Arg Arg Thr
185 190 195

Lys Arg Thr Arg Arg Pro Gln Pro Leu Thr
200 205

<210> 24
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 24
cagtacgtga gggaccaggg cgccatga 28

<210> 25
<211> 24
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 25
ccggtgacct gcacgtgctt gcca 24

<210> 26
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<220>
<221> unsure
<222> 21
<223> unknown base

<400> 26
gcggatctgc cgcctgctca nctggtcggt catggcgccc t 41

<210> 27
<211> 2479
<212> DNA
<213> Homo Sapien

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ttgcacatgg aggacagcag caaagagggc aacacaggct gataagacca 100

gagacagcag ggagattatt ttaccatacg ccctcaggac gttccctcta 150

gctggagttc tggacttcaa cagaacccca tccagtcatt ttgattttgc 200

tgtttatttt ttttttcttt ttctttttcc caccacattg tattttattt 250

ccgtacttca gaaatgggcc tacagaccac aaagtggccc agccatgggg 300

ctttttttcct gaagtcttgg cttatcattt ccctggggct ctactcacag 350

gtgtccaaac tcctggcctg ccctagtgtg tgccgctgcg acaggaactt 400

tgtctactgt aatgagcgaa gcttgacctc agtgcctctt gggatcccgg 450

agggcgtaac cgtactctac ctccacaaca accaaattaa taatgctgga 500

tttcctgcag aactgcacaa tgtacagtcg gtgcacacgg tctacctgta 550

tggcaaccaa ctggacgaat tccccatgaa ccttcccaag aatgtcagag 600

ttctccattt gcaggaaaac aatattcaga ccatttcacg ggctgctctt 650

gcccagctct tgaagcttga agagctgcac ctggatgaca actccatatc 700

cacagtgggg gtggaagacg gggccttccg ggaggctatt agcctcaaat 750

tgttgttttt gtctaagaat cacctgagca gtgtgcctgt tgggcttcct 800

gtggacttgc aagagctgag agtggatgaa aatcgaattg ctgtcatatc 850

cgacatggcc ttccagaatc tcacgagctt ggagcgtctt attgtggacg 900

ggaacctcct gaccaacaag ggtatcgccg agggcacctt cagccatctc 950

accaagctca aggaattttc aattgtacgt aattcgctgt cccaccctcc 1000

tcccgatctc ccaggtacgc atctgatcag gctctatttg caggacaacc 1050

agataaacca cattcctttg acagccttct caaatctgcg taagctggaa 1100

cggctggata tatccaacaa ccaactgcgg atgctgactc aaggggtttt 1150

tgataatctc tccaacctga agcagctcac tgctcggaat aacccttggt 1200

tttgtgactg cagtattaaa tgggtcacag aatggctcaa atatatccct 1250

tcatctctca acgtgcgggg tttcatgtgc caaggtcctg aacaagtccg 1300

ggggatggcc gtcagggaat taaatatgaa tcttttgtcc tgtcccacca 1350

cgacccccgg cctgcctctc ttcaccccag ccccaagtac agcttctccg 1400

accactcagc ctcccaccct ctctattcca aaccctagca gaagctacac 1450

gcctccaact cctaccacat cgaaacttcc cacgattcct gactgggatg 1500

gcagagaaag agtgacccca cctatttctg aacggatcca gctctctatc 1550

cattttgtga atgatacttc cattcaagtc agctggctct ctctcttcac 1600

cgtgatggca tacaaactca catgggtgaa aatgggccac agtttagtag 1650

ggggcatcgt tcaggagcgc atagtcagcg gtgagaagca acacctgagc 1700

ctggttaact tagagccccg atccacctat cggatttgtt tagtgccact 1750

ggatgctttt aactaccgcg cggtagaaga caccatttgt tcagaggcca 1800

ccacccatgc ctcctatctg aacaacggca gcaacacagc gtccagccat 1850

gagcagacga cgtcccacag catgggctcc ccctttctgc tggcgggctt 1900

gatcgggggc gcggtgatat ttgtgctggt ggtcttgctc agcgtctttt 1950

gctggcatat gcacaaaaag gggcgctaca cctcccagaa gtggaaatac 2000

aaccggggcc ggcggaaaga tgattattgc gaggcaggca ccaagaagga 2050

caactccatc ctggagatga cagaaaccag ttttcagatc gtctccttaa 2100

ataacgatca actccttaaa ggagatttca gactgcagcc catttacacc 2150

ccaaatgggg gcattaatta cacagactgc catatcccca acaacatgcg 2200

atactgcaac agcagcgtgc cagacctgga gcactgccat acgtgacagc 2250

cagaggccca gcgttatcaa ggcggacaat tagactcttg agaacacact 2300

cgtgtgtgca cataaagaca cgcagattac atttgataaa tgttacacag 2350

atgcatttgt gcatttgaat actctgtaat ttatacggtg tactatataa 2400

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<210> 28
<211> 660
<212> PRT
<213> Homo Sapien

<400> 28

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 Leu Lys Ser Trp Leu Ile Ile Ser Leu Gly Leu Tyr Ser Gln Val
                20                  25                  30

 Ser Lys Leu Leu Ala Cys Pro Ser Val Cys Arg Cys Asp Arg Asn
                35                  40                  45

 Phe Val Tyr Cys Asn Glu Arg Ser Leu Thr Ser Val Pro Leu Gly
                50                  55                  60

 Ile Pro Glu Gly Val Thr Val Leu Tyr Leu His Asn Asn Gln Ile
                65                  70                  75

 Asn Asn Ala Gly Phe Pro Ala Glu Leu His Asn Val Gln Ser Val
                80                  85                  90

 His Thr Val Tyr Leu Tyr Gly Asn Gln Leu Asp Glu Phe Pro Met
                95                 100                 105

 Asn Leu Pro Lys Asn Val Arg Val Leu His Leu Gln Glu Asn Asn
               110                 115                 120

 Ile Gln Thr Ile Ser Arg Ala Ala Leu Ala Gln Leu Leu Lys Leu
               125                 130                 135

 Glu Glu Leu His Leu Asp Asp Asn Ser Ile Ser Thr Val Gly Val
               140                 145                 150

 Glu Asp Gly Ala Phe Arg Glu Ala Ile Ser Leu Lys Leu Leu Phe
               155                 160                 165

 Leu Ser Lys Asn His Leu Ser Ser Val Pro Val Gly Leu Pro Val
               170                 175                 180

 Asp Leu Gln Glu Leu Arg Val Asp Glu Asn Arg Ile Ala Val Ile
               185                 190                 195

 Ser Asp Met Ala Phe Gln Asn Leu Thr Ser Leu Glu Arg Leu Ile
               200                 205                 210

 Val Asp Gly Asn Leu Leu Thr Asn Lys Gly Ile Ala Glu Gly Thr
               215                 220                 225

 Phe Ser His Leu Thr Lys Leu Lys Glu Phe Ser Ile Val Arg Asn
               230                 235                 240

 Ser Leu Ser His Pro Pro Pro Asp Leu Pro Gly Thr His Leu Ile
               245                 250                 255

 Arg Leu Tyr Leu Gln Asp Asn Gln Ile Asn His Ile Pro Leu Thr
               260                 265                 270

 Ala Phe Ser Asn Leu Arg Lys Leu Glu Arg Leu Asp Ile Ser Asn
               275                 280                 285
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Asn Gln Leu Arg Met Leu Thr Gln Gly Val Phe Asp Asn Leu Ser
                290                 295                 300

Asn Leu Lys Gln Leu Thr Ala Arg Asn Asn Pro Trp Phe Cys Asp
                305                 310                 315

Cys Ser Ile Lys Trp Val Thr Glu Trp Leu Lys Tyr Ile Pro Ser
                320                 325                 330

Ser Leu Asn Val Arg Gly Phe Met Cys Gln Gly Pro Glu Gln Val
                335                 340                 345

Arg Gly Met Ala Val Arg Glu Leu Asn Met Asn Leu Leu Ser Cys
                350                 355                 360

Pro Thr Thr Thr Pro Gly Leu Pro Leu Phe Thr Pro Ala Pro Ser
                365                 370                 375

Thr Ala Ser Pro Thr Thr Gln Pro Pro Thr Leu Ser Ile Pro Asn
                380                 385                 390

Pro Ser Arg Ser Tyr Thr Pro Pro Thr Pro Thr Thr Ser Lys Leu
                395                 400                 405

Pro Thr Ile Pro Asp Trp Asp Gly Arg Glu Arg Val Thr Pro Pro
                410                 415                 420

Ile Ser Glu Arg Ile Gln Leu Ser Ile His Phe Val Asn Asp Thr
                425                 430                 435

Ser Ile Gln Val Ser Trp Leu Ser Leu Phe Thr Val Met Ala Tyr
                440                 445                 450

Lys Leu Thr Trp Val Lys Met Gly His Ser Leu Val Gly Gly Ile
                455                 460                 465

Val Gln Glu Arg Ile Val Ser Gly Glu Lys Gln His Leu Ser Leu
                470                 475                 480

Val Asn Leu Glu Pro Arg Ser Thr Tyr Arg Ile Cys Leu Val Pro
                485                 490                 495

Leu Asp Ala Phe Asn Tyr Arg Ala Val Glu Asp Thr Ile Cys Ser
                500                 505                 510

Glu Ala Thr Thr His Ala Ser Tyr Leu Asn Asn Gly Ser Asn Thr
                515                 520                 525

Ala Ser Ser His Glu Gln Thr Thr Ser His Ser Met Gly Ser Pro
                530                 535                 540

Phe Leu Leu Ala Gly Leu Ile Gly Gly Ala Val Ile Phe Val Leu
                545                 550                 555

Val Val Leu Leu Ser Val Phe Cys Trp His Met His Lys Lys Gly
                560                 565                 570

Arg Tyr Thr Ser Gln Lys Trp Lys Tyr Asn Arg Gly Arg Arg Lys
                575                 580                 585

Asp Asp Tyr Cys Glu Ala Gly Thr Lys Lys Asp Asn Ser Ile Leu
                590                 595                 600
```

Glu Met Thr Glu Thr Ser Phe Gln Ile Val Ser Leu Asn Asn Asp
605 610 615

Gln Leu Leu Lys Gly Asp Phe Arg Leu Gln Pro Ile Tyr Thr Pro
620 625 630

Asn Gly Gly Ile Asn Tyr Thr Asp Cys His Ile Pro Asn Asn Met
635 640 645

Arg Tyr Cys Asn Ser Ser Val Pro Asp Leu Glu His Cys His Thr
650 655 660

<210> 29
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 29
cggtctacct gtatggcaac c 21

<210> 30
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 30
gcaggacaac cagataaacc ac 22

<210> 31
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 31
acgcagattt gagaaggctg tc 22

<210> 32
<211> 46
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 32
ttcacgggct gctcttgccc agctcttgaa gcttgaagag ctgcac 46

<210> 33
<211> 3449
<212> DNA
<213> Homo Sapien

<400> 33

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gctccgtcct cgcctcccac gagcgatccc cgaggagagc cgcggccctc 100

ggcgaggcga agaggccgac gaggaagacc cgggtggctg cgcccctgcc 150

tcgcttccca ggcgccggcg gctgcagcct tgcccctctt gctcgccttg 200

aaaatggaaa agatgctcgc aggctgcttt ctgctgatcc tcggacagat 250

cgtcctcctc cctgccgagg ccagggagcg gtcacgtggg aggtccatct 300

ctaggggcag acacgctcgg acccacccgc agacggccct tctggagagt 350

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gaagcagagg gggcccggcc cctgagggag aatgtgccac gggtcataat 700

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gtgccatgga ggaccacaac tgtgagcagc tctgtgtgaa tgtgccgggc 1100

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gaggtgtgtg gctgtggact actgtgcctc agaaaaccac ggatgtgaac 1200

atgagtgtgt aaatgctgat ggctcctacc tttgccagtg ccatgaagga 1250

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actactgccg ctgccaccgt ggctacactc tggaccccaa tggcaaaacc 1400

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accatggctg tgaacacatt tgtgtgaaca gtgacgactc atacacgtgc 1850

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gaaggatgtc tgcaaatcaa cccaccatgg ctgcgaacac atttgtgtta 1950

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tgaagcagtt tgtcactgga attatagatt ccttgacaat ttcccccaaa 2150

gccgctcgag tggggctgct ccagtattcc acacaggtcc acacagagtt 2200

cactctgaga aacttcaact cagccaaaga catgaaaaaa gccgtggccc 2250

acatgaaata catgggaaag ggctctatga ctgggctggc cctgaaacac 2300

atgtttgaga gaagttttac ccaaggagaa ggggccaggc ccctttccac 2350

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cttgatatat gtatatggat gtatgcataa aatcatagga catatgtact 3400

tgtggaacaa gttggatttt ttatacaata ttaaaattca ccacttcag 3449

<210> 34
<211> 915
<212> PRT
<213> Homo Sapien

<400> 34

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Met Glu Lys Met Leu Ala Gly Cys Phe Leu Leu Ile Leu Gly Gln
  1               5                  10                  15

Ile Val Leu Leu Pro Ala Glu Ala Arg Glu Arg Ser Arg Gly Arg
             20                  25                  30

Ser Ile Ser Arg Gly Arg His Ala Arg Thr His Pro Gln Thr Ala
         35                  40                  45

Leu Leu Glu Ser Ser Cys Glu Asn Lys Arg Ala Asp Leu Val Phe
     50                  55                  60

Ile Ile Asp Ser Ser Arg Ser Val Asn Thr His Asp Tyr Ala Lys
 65                  70                  75

Val Lys Glu Phe Ile Val Asp Ile Leu Gln Phe Leu Asp Ile Gly
             80                  85                  90

Pro Asp Val Thr Arg Val Gly Leu Leu Gln Tyr Gly Ser Thr Val
         95                 100                 105

Lys Asn Glu Phe Ser Leu Lys Thr Phe Lys Arg Lys Ser Glu Val
    110                 115                 120

Glu Arg Ala Val Lys Arg Met Arg His Leu Ser Thr Gly Thr Met
    125                 130                 135

Thr Gly Leu Ala Ile Gln Tyr Ala Leu Asn Ile Ala Phe Ser Glu
    140                 145                 150

Ala Glu Gly Ala Arg Pro Leu Arg Glu Asn Val Pro Arg Val Ile
    155                 160                 165

Met Ile Val Thr Asp Gly Arg Pro Gln Asp Ser Val Ala Glu Val
    170                 175                 180

Ala Ala Lys Ala Arg Asp Thr Gly Ile Leu Ile Phe Ala Ile Gly
    185                 190                 195

Val Gly Gln Val Asp Phe Asn Thr Leu Lys Ser Ile Gly Ser Glu
    200                 205                 210

Pro His Glu Asp His Val Phe Leu Val Ala Asn Phe Ser Gln Ile
    215                 220                 225
```

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Glu Thr Leu Thr Ser Val Phe Gln Lys Lys Leu Cys Thr Ala His
                230                 235                 240

Met Cys Ser Thr Leu Glu His Asn Cys Ala His Phe Cys Ile Asn
                245                 250                 255

Ile Pro Gly Ser Tyr Val Cys Arg Cys Lys Gln Gly Tyr Ile Leu
                260                 265                 270

Asn Ser Asp Gln Thr Thr Cys Arg Ile Gln Asp Leu Cys Ala Met
                275                 280                 285

Glu Asp His Asn Cys Glu Gln Leu Cys Val Asn Val Pro Gly Ser
                290                 295                 300

Phe Val Cys Gln Cys Tyr Ser Gly Tyr Ala Leu Ala Glu Asp Gly
                305                 310                 315

Lys Arg Cys Val Ala Val Asp Tyr Cys Ala Ser Glu Asn His Gly
                320                 325                 330

Cys Glu His Glu Cys Val Asn Ala Asp Gly Ser Tyr Leu Cys Gln
                335                 340                 345

Cys His Glu Gly Phe Ala Leu Asn Pro Asp Glu Lys Thr Cys Thr
                350                 355                 360

Arg Ile Asn Tyr Cys Ala Leu Asn Lys Pro Gly Cys Glu His Glu
                365                 370                 375

Cys Val Asn Met Glu Glu Ser Tyr Tyr Cys Arg Cys His Arg Gly
                380                 385                 390

Tyr Thr Leu Asp Pro Asn Gly Lys Thr Cys Ser Arg Val Asp His
                395                 400                 405

Cys Ala Gln Gln Asp His Gly Cys Glu Gln Leu Cys Leu Asn Thr
                410                 415                 420

Glu Asp Ser Phe Val Cys Gln Cys Ser Glu Gly Phe Leu Ile Asn
                425                 430                 435

Glu Asp Leu Lys Thr Cys Ser Arg Val Asp Tyr Cys Leu Leu Ser
                440                 445                 450

Asp His Gly Cys Glu Tyr Ser Cys Val Asn Met Asp Arg Ser Phe
                455                 460                 465

Ala Cys Gln Cys Pro Glu Gly His Val Leu Arg Ser Asp Gly Lys
                470                 475                 480

Thr Cys Ala Lys Leu Asp Ser Cys Ala Leu Gly Asp His Gly Cys
                485                 490                 495

Glu His Ser Cys Val Ser Ser Glu Asp Ser Phe Val Cys Gln Cys
                500                 505                 510

Phe Glu Gly Tyr Ile Leu Arg Glu Asp Gly Lys Thr Cys Arg Arg
                515                 520                 525

Lys Asp Val Cys Gln Ala Ile Asp His Gly Cys Glu His Ile Cys
                530                 535                 540
```

```
Val Asn Ser Asp Asp Ser Tyr Thr Cys Glu Cys Leu Glu Gly Phe
                545                 550                 555

Arg Leu Ala Glu Asp Gly Lys Arg Cys Arg Arg Lys Asp Val Cys
                560                 565                 570

Lys Ser Thr His His Gly Cys Glu His Ile Cys Val Asn Asn Gly
                575                 580                 585

Asn Ser Tyr Ile Cys Lys Cys Ser Glu Gly Phe Val Leu Ala Glu
                590                 595                 600

Asp Gly Arg Arg Cys Lys Lys Cys Thr Glu Gly Pro Ile Asp Leu
                605                 610                 615

Val Phe Val Ile Asp Gly Ser Lys Ser Leu Gly Glu Glu Asn Phe
                620                 625                 630

Glu Val Val Lys Gln Phe Val Thr Gly Ile Ile Asp Ser Leu Thr
                635                 640                 645

Ile Ser Pro Lys Ala Ala Arg Val Gly Leu Leu Gln Tyr Ser Thr
                650                 655                 660

Gln Val His Thr Glu Phe Thr Leu Arg Asn Phe Asn Ser Ala Lys
                665                 670                 675

Asp Met Lys Lys Ala Val Ala His Met Lys Tyr Met Gly Lys Gly
                680                 685                 690

Ser Met Thr Gly Leu Ala Leu Lys His Met Phe Glu Arg Ser Phe
                695                 700                 705

Thr Gln Gly Glu Gly Ala Arg Pro Leu Ser Thr Arg Val Pro Arg
                710                 715                 720

Ala Ala Ile Val Phe Thr Asp Gly Arg Ala Gln Asp Asp Val Ser
                725                 730                 735

Glu Trp Ala Ser Lys Ala Lys Ala Asn Gly Ile Thr Met Tyr Ala
                740                 745                 750

Val Gly Val Gly Lys Ala Ile Glu Glu Glu Leu Gln Glu Ile Ala
                755                 760                 765

Ser Glu Pro Thr Asn Lys His Leu Phe Tyr Ala Glu Asp Phe Ser
                770                 775                 780

Thr Met Asp Glu Ile Ser Glu Lys Leu Lys Lys Gly Ile Cys Glu
                785                 790                 795

Ala Leu Glu Asp Ser Asp Gly Arg Gln Asp Ser Pro Ala Gly Glu
                800                 805                 810

Leu Pro Lys Thr Val Gln Gln Pro Thr Glu Ser Glu Pro Val Thr
                815                 820                 825

Ile Asn Ile Gln Asp Leu Leu Ser Cys Ser Asn Phe Ala Val Gln
                830                 835                 840

His Arg Tyr Leu Phe Glu Glu Asp Asn Leu Leu Arg Ser Thr Gln
                845                 850                 855
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Lys Leu Ser His Ser Thr Lys Pro Ser Gly Ser Pro Leu Glu Glu
860 865 870

Lys His Asp Gln Cys Lys Cys Glu Asn Leu Ile Met Phe Gln Asn
875 880 885

Leu Ala Asn Glu Glu Val Arg Lys Leu Thr Gln Arg Leu Glu Glu
890 895 900

Met Thr Gln Arg Met Glu Ala Leu Glu Asn Arg Leu Arg Tyr Arg
905 910 915

<210> 35
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 35
gtgaccctgg ttgtgaatac tcc 23

<210> 36
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 36
acagccatgg tctatagctt gg 22

<210> 37
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 37
gcctgtcagt gtcctgaggg acacgtgctc cgcagcgatg ggaag 45

<210> 38
<211> 1813
<212> DNA
<213> Homo Sapien

<400> 38
ggagccgccc tgggtgtcag cggctcggct cccgcgcacg ctccggccgt 50

cgcgcagcct cggcacctgc aggtccgtgc gtcccgcggc tggcgccccc 100

gactccgtcc cggccaggga gggccatgat ttccctcccg gggcccctgg 150

tgaccaactt gctgcggttt ttgttcctgg ggctgagtgc cctcgcgccc 200

ccctcgcggg cccagctgca actgcacttg cccgccaacc ggttgcaggc 250

ggtggaggga ggggaagtgg tgcttccagc gtggtacacc ttgcacgggg 300

aggtgtcttc atcccagcca tgggaggtgc cctttgtgat gtggttcttc 350

aaacagaaag aaaaggagga tcaggtgttg tcctacatca atggggtcac 400

aacaagcaaa cctggagtat ccttggtcta ctccatgccc tcccggaacc 450

tgtccctgcg gctggagggt ctccaggaga aagactctgg cccctacagc 500

tgctccgtga atgtgcaaga caaacaaggc aaatctaggg gccacagcat 550

caaaacctta gaactcaatg tactggttcc tccagctcct ccatcctgcc 600

gtctccaggg tgtgccccat gtgggggcaa acgtgaccct gagctgccag 650

tctccaagga gtaagcccgc tgtccaatac cagtgggatc ggcagcttcc 700

atccttccag actttctttg caccagcatt agatgtcatc cgtgggtctt 750

taagcctcac caacctttcg tcttccatgg ctggagtcta tgtctgcaag 800

gcccacaatg aggtgggcac tgcccaatgt aatgtgacgc tggaagtgag 850

cacagggcct ggagctgcag tggttgctgg agctgttgtg ggtaccctgg 900

ttggactggg gttgctggct gggctggtcc tcttgtacca ccgccggggc 950

aaggccctgg aggagccagc caatgatatc aaggaggatg ccattgctcc 1000

ccggaccctg ccctggccca agagctcaga cacaatctcc aagaatggga 1050

ccctttcctc tgtcacctcc gcacgagccc tccggccacc ccatggccct 1100

cccaggcctg gtgcattgac ccccacgccc agtctctcca gccaggccct 1150

gccctcacca agactgccca cgacagatgg ggcccaccct caaccaatat 1200

cccccatccc tggtggggtt tcttcctctg gcttgagccg catgggtgct 1250

gtgcctgtga tggtgcctgc ccagagtcaa gctggctctc tggtatgatg 1300

accccaccac tcattggcta aaggatttgg ggtctctcct tcctataagg 1350

gtcacctcta gcacagaggc ctgagtcatg ggaaagagtc acactcctga 1400

cccttagtac tctgccccca cctctcttta ctgtgggaaa accatctcag 1450

taagacctaa gtgtccagga gacagaagga gaagaggaag tggatctgga 1500

attgggagga gcctccaccc acccctgact cctccttatg aagccagctg 1550

ctgaaattag ctactcacca agagtgaggg gcagagactt ccagtcactg 1600

agtctcccag gccccttga tctgtacccc acccctatct aacaccaccc 1650

ttggctccca ctccagctcc ctgtattgat ataacctgtc aggctggctt 1700

ggttaggttt tactggggca gaggataggg aatctcttat taaaactaac 1750

atgaaatatg tgttgttttc atttgcaaat ttaaataaag atacataatg 1800

tttgtatgaa aaa 1813

<210> 39

<211> 390
<212> PRT
<213> Homo Sapien

<400> 39

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 Met Ile Ser Leu Pro Gly Pro Leu Val Thr Asn Leu Leu Arg Phe
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 Leu Phe Leu Gly Leu Ser Ala Leu Ala Pro Pro Ser Arg Ala Gln
                20                  25                  30

 Leu Gln Leu His Leu Pro Ala Asn Arg Leu Gln Ala Val Glu Gly
                35                  40                  45

 Gly Glu Val Val Leu Pro Ala Trp Tyr Thr Leu His Gly Glu Val
                50                  55                  60

 Ser Ser Ser Gln Pro Trp Glu Val Pro Phe Val Met Trp Phe Phe
                65                  70                  75

 Lys Gln Lys Glu Lys Glu Asp Gln Val Leu Ser Tyr Ile Asn Gly
                80                  85                  90

 Val Thr Thr Ser Lys Pro Gly Val Ser Leu Val Tyr Ser Met Pro
                95                 100                 105

 Ser Arg Asn Leu Ser Leu Arg Leu Glu Gly Leu Gln Glu Lys Asp
               110                 115                 120

 Ser Gly Pro Tyr Ser Cys Ser Val Asn Val Gln Asp Lys Gln Gly
               125                 130                 135

 Lys Ser Arg Gly His Ser Ile Lys Thr Leu Glu Leu Asn Val Leu
               140                 145                 150

 Val Pro Pro Ala Pro Pro Ser Cys Arg Leu Gln Gly Val Pro His
               155                 160                 165

 Val Gly Ala Asn Val Thr Leu Ser Cys Gln Ser Pro Arg Ser Lys
               170                 175                 180

 Pro Ala Val Gln Tyr Gln Trp Asp Arg Gln Leu Pro Ser Phe Gln
               185                 190                 195

 Thr Phe Phe Ala Pro Ala Leu Asp Val Ile Arg Gly Ser Leu Ser
               200                 205                 210

 Leu Thr Asn Leu Ser Ser Ser Met Ala Gly Val Tyr Val Cys Lys
               215                 220                 225

 Ala His Asn Glu Val Gly Thr Ala Gln Cys Asn Val Thr Leu Glu
               230                 235                 240

 Val Ser Thr Gly Pro Gly Ala Ala Val Val Ala Gly Ala Val Val
               245                 250                 255

 Gly Thr Leu Val Gly Leu Gly Leu Leu Ala Gly Leu Val Leu Leu
               260                 265                 270

 Tyr His Arg Arg Gly Lys Ala Leu Glu Glu Pro Ala Asn Asp Ile
               275                 280                 285

 Lys Glu Asp Ala Ile Ala Pro Arg Thr Leu Pro Trp Pro Lys Ser
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290 295 300

Ser Asp Thr Ile Ser Lys Asn Gly Thr Leu Ser Ser Val Thr Ser
305 310 315

Ala Arg Ala Leu Arg Pro Pro His Gly Pro Pro Arg Pro Gly Ala
320 325 330

Leu Thr Pro Thr Pro Ser Leu Ser Ser Gln Ala Leu Pro Ser Pro
335 340 345

Arg Leu Pro Thr Thr Asp Gly Ala His Pro Gln Pro Ile Ser Pro
350 355 360

Ile Pro Gly Gly Val Ser Ser Ser Gly Leu Ser Arg Met Gly Ala
365 370 375

Val Pro Val Met Val Pro Ala Gln Ser Gln Ala Gly Ser Leu Val
380 385 390

<210> 40
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 40
agggtctcca ggagaaagac tc 22

<210> 41
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 41
attgtgggcc ttgcagacat agac 24

<210> 42
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 42
ggccacagca tcaaaacctt agaactcaat gtactggttc ctccagctcc 50

<210> 43
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 43
gtgtgacaca gcgtgggc 18

<210> 44
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 44
gaccggcagg cttctgcg 18

<210> 45
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 45
cagcagcttc agccaccagg agtgg 25

<210> 46
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 46
ctgagccgtg ggctgcagtc tcgc 24

<210> 47
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 47
ccgactacga ctggttcttc atcatgcagg atgacacata tgtgc 45

<210> 48
<211> 2822
<212> DNA
<213> Homo Sapien

<400> 48
cgccaccact gcggccaccg ccaatgaaac gcctcccgct cctagtggtt 50

ttttccactt tgttgaattg ttcctatact caaaattgca ccaagacacc 100

ttgtctccca aatgcaaaat gtgaaatacg caatggaatt gaagcctgct 150

attgcaacat gggattttca ggaaatggtg tcacaatttg tgaagatgat 200

aatgaatgtg gaaatttaac tcagtcctgt ggcgaaaatg ctaattgcac 250

taacacagaa ggaagttatt attgtatgtg tgtacctggc ttcagatcca 300

gcagtaacca agacaggttt atcactaatg atggaaccgt ctgtatagaa 350

aatgtgaatg caaactgcca tttagataat gtctgtatag ctgcaaatat 400

taataaaact ttaacaaaaa tcagatccat aaaagaacct gtggctttgc 450

tacaagaagt ctatagaaat tctgtgacag atctttcacc aacagatata 500

attacatata tagaaatatt agctgaatca tcttcattac taggttacaa 550

gaacaacact atctcagcca aggacaccct ttctaactca actcttactg 600

aatttgtaaa aaccgtgaat aattttgttc aaagggatac atttgtagtt 650

tgggacaagt tatctgtgaa tcataggaga acacatctta caaaactcat 700

gcacactgtt gaacaagcta ctttaaggat atcccagagc ttccaaaaga 750

ccacagagtt tgatacaaat tcaacggata tagctctcaa agttttcttt 800

tttgattcat ataacatgaa acatattcat cctcatatga atatggatgg 850

agactacata aatatatttc caaagagaaa agctgcatat gattcaaatg 900

gcaatgttgc agttgcattt ttatattata agagtattgg tcctttgctt 950

tcatcatctg acaacttctt attgaaacct caaaattatg ataattctga 1000

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ccatatgcat ttttaccttc tggttcttca gtgaaattca aagcaccagg 1400

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tctcggcacc acctggatct ttggggttct ccatgttgtg cacgcatcag 1950

tggttacagc ttacctcttc acagtcagca atgctttcca ggggatgttc 2000

attttttat tcctgtgtgt tttatctaga aagattcaag aagaatatta 2050

cagattgttc aaaaatgtcc cctgttgttt tggatgttta aggtaaacat 2100

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ggatgaccaa tgtataaaaa tgactcatca aattatccaa ttattaacta 2200

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gtagataata aggtaaaatt atgtatcata tagatatact atgtttttct 2300

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ctccattaca gaaagtggaa cataagagaa tgaaggggca gaatatcaaa 2550

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agactagctg agaaattgtt gacataaaat aaagaattga agaaacacat 2650

tttaccattt tgtgaattgt tctgaactta aatgtccact aaaacaactt 2700

agacttctgt ttgctaaatc tgtttctttt tctaatattc taaaaaaaaa 2750

aaaaaggttt acctccacaa attgaaaaaa aaaaaaaaaa aaaaaaaaaa 2800

aaaaaaaaaa aaaaaaaaaa aa 2822

<210> 49
<211> 690
<212> PRT
<213> Homo Sapien

<400> 49

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Met Lys Arg Leu Pro Leu Leu Val Val Phe Ser Thr Leu Leu Asn
  1               5                  10                  15

Cys Ser Tyr Thr Gln Asn Cys Thr Lys Thr Pro Cys Leu Pro Asn
             20                  25                  30

Ala Lys Cys Glu Ile Arg Asn Gly Ile Glu Ala Cys Tyr Cys Asn
             35                  40                  45

Met Gly Phe Ser Gly Asn Gly Val Thr Ile Cys Glu Asp Asp Asn
             50                  55                  60

Glu Cys Gly Asn Leu Thr Gln Ser Cys Gly Glu Asn Ala Asn Cys
             65                  70                  75

Thr Asn Thr Glu Gly Ser Tyr Tyr Cys Met Cys Val Pro Gly Phe
             80                  85                  90
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Arg Ser Ser Ser Asn Gln Asp Arg Phe Ile Thr Asn Asp Gly Thr
 95                 100                 105

Val Cys Ile Glu Asn Val Asn Ala Asn Cys His Leu Asp Asn Val
110                 115                 120

Cys Ile Ala Ala Asn Ile Asn Lys Thr Leu Thr Lys Ile Arg Ser
125                 130                 135

Ile Lys Glu Pro Val Ala Leu Leu Gln Glu Val Tyr Arg Asn Ser
140                 145                 150

Val Thr Asp Leu Ser Pro Thr Asp Ile Ile Thr Tyr Ile Glu Ile
155                 160                 165

Leu Ala Glu Ser Ser Ser Leu Leu Gly Tyr Lys Asn Asn Thr Ile
170                 175                 180

Ser Ala Lys Asp Thr Leu Ser Asn Ser Thr Leu Thr Glu Phe Val
185                 190                 195

Lys Thr Val Asn Asn Phe Val Gln Arg Asp Thr Phe Val Val Trp
200                 205                 210

Asp Lys Leu Ser Val Asn His Arg Arg Thr His Leu Thr Lys Leu
215                 220                 225

Met His Thr Val Glu Gln Ala Thr Leu Arg Ile Ser Gln Ser Phe
230                 235                 240

Gln Lys Thr Thr Glu Phe Asp Thr Asn Ser Thr Asp Ile Ala Leu
245                 250                 255

Lys Val Phe Phe Phe Asp Ser Tyr Asn Met Lys His Ile His Pro
260                 265                 270

His Met Asn Met Asp Gly Asp Tyr Ile Asn Ile Phe Pro Lys Arg
275                 280                 285

Lys Ala Ala Tyr Asp Ser Asn Gly Asn Val Ala Val Ala Phe Leu
290                 295                 300

Tyr Tyr Lys Ser Ile Gly Pro Leu Leu Ser Ser Ser Asp Asn Phe
305                 310                 315

Leu Leu Lys Pro Gln Asn Tyr Asp Asn Ser Glu Glu Glu Glu Arg
320                 325                 330

Val Ile Ser Ser Val Ile Ser Val Ser Met Ser Ser Asn Pro Pro
335                 340                 345

Thr Leu Tyr Glu Leu Glu Lys Ile Thr Phe Thr Leu Ser His Arg
350                 355                 360

Lys Val Thr Asp Arg Tyr Arg Ser Leu Cys Ala Phe Trp Asn Tyr
365                 370                 375

Ser Pro Asp Thr Met Asn Gly Ser Trp Ser Ser Glu Gly Cys Glu
380                 385                 390

Leu Thr Tyr Ser Asn Glu Thr His Thr Ser Cys Arg Cys Asn His
395                 400                 405
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Leu Thr His Phe Ala Ile Leu Met Ser Ser Gly Pro Ser Ile Gly
410 415 420

Ile Lys Asp Tyr Asn Ile Leu Thr Arg Ile Thr Gln Leu Gly Ile
425 430 435

Ile Ile Ser Leu Ile Cys Leu Ala Ile Cys Ile Phe Thr Phe Trp
440 445 450

Phe Phe Ser Glu Ile Gln Ser Thr Arg Thr Thr Ile His Lys Asn
455 460 465

Leu Cys Cys Ser Leu Phe Leu Ala Glu Leu Val Phe Leu Val Gly
470 475 480

Ile Asn Thr Asn Thr Asn Lys Leu Phe Cys Ser Ile Ile Ala Gly
485 490 495

Leu Leu His Tyr Phe Phe Leu Ala Ala Phe Ala Trp Met Cys Ile
500 505 510

Glu Gly Ile His Leu Tyr Leu Ile Val Val Gly Val Ile Tyr Asn
515 520 525

Lys Gly Phe Leu His Lys Asn Phe Tyr Ile Phe Gly Tyr Leu Ser
530 535 540

Pro Ala Val Val Val Gly Phe Ser Ala Ala Leu Gly Tyr Arg Tyr
545 550 555

Tyr Gly Thr Thr Lys Val Cys Trp Leu Ser Thr Glu Asn Asn Phe
560 565 570

Ile Trp Ser Phe Ile Gly Pro Ala Cys Leu Ile Ile Leu Val Asn
575 580 585

Leu Leu Ala Phe Gly Val Ile Ile Tyr Lys Val Phe Arg His Thr
590 595 600

Ala Gly Leu Lys Pro Glu Val Ser Cys Phe Glu Asn Ile Arg Ser
605 610 615

Cys Ala Arg Gly Ala Leu Ala Leu Leu Phe Leu Leu Gly Thr Thr
620 625 630

Trp Ile Phe Gly Val Leu His Val Val His Ala Ser Val Val Thr
635 640 645

Ala Tyr Leu Phe Thr Val Ser Asn Ala Phe Gln Gly Met Phe Ile
650 655 660

Phe Leu Phe Leu Cys Val Leu Ser Arg Lys Ile Gln Glu Glu Tyr
665 670 675

Tyr Arg Leu Phe Lys Asn Val Pro Cys Cys Phe Gly Cys Leu Arg
680 685 690

<210> 50
<211> 589
<212> DNA
<213> Homo Sapien

<220>

<221> unsure
<222> 61
<223> unknown base

<400> 50
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atttccaaag ngaaaagccg gcatatggat tcaaatggca atgttgcagt 100

tgcattttta tattataaga gtattggtcc ctttgctttc atcatctgac 150

aacttcttat tgaaacctca aaattatgat aattctgaag aggaggaaag 200

agtcatatct tcagtaattt cagtctcaat gagctcaaac ccacccacat 250

tatatgaact tgaaaaaata acatttacat taagtcatcg aaaggtcaca 300

gataggtata ggagtctatg tggcattttg gaatactcac ctgataccat 350

gaatggcagc tggtcttcag agggctgtga gctgacatac tcaaatgaga 400

cccacacctc atgccgctgt aatcacctga cacattttgc aattttgatg 450

tcctctggtc cttccattgg tattaaagat tataatattc ttacaaggat 500

cactcaacta ggaataatta tttcactgat ttgtcttgcc atatgcattt 550

ttaccttctg gttcttcagt gaaattcaaa gcaccagga 589

<210> 51
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 51
ggtaatgagc tccattacag 20

<210> 52
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 52
ggagtagaaa gcgcatgg 18

<210> 53
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 53
cacctgatac catgaatggc ag 22

<210> 54

<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 54
cgagctcgaa ttaattcg 18

<210> 55
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 55
ggatctcctg agctcagg 18

<210> 56
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 56
cctagttgag tgatccttgt aag 23

<210> 57
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 57
atgagaccca cacctcatgc cgctgtaatc acctgacaca ttttgcaatt 50

<210> 58
<211> 2137
<212> DNA
<213> Homo Sapien

<400> 58
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gaaacccggc cgctaagcga ggcctcctcc tcccgcagat ccgaacggcc 100

tgggcggggt caccccggct gggacaagaa gccgccgcct gcctgcccgg 150

gcccggggag ggggctgggg ctggggccgg aggcggggtg tgagtgggtg 200

tgtgcggggg gcggaggctt gatgcaatcc cgataagaaa tgctcgggtg 250

tcttgggcac ctacccgtgg ggcccgtaag gcgctactat ataaggctgc 300

cggcccggag ccgccgcgcc gtcagagcag gagcgctgcg tccaggatct 350

agggccacga ccatcccaac ccggcactca cagccccgca gcgcatcccg 400

gtcgccgccc agcctcccgc acccccatcg ccggagctgc gccgagagcc 450

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ttcagagttt tccattggca gtgccagttt ctagccaata gacttgtctg 1300

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ttctgctccc tcgaggttgc tggacaagct gctgcactgt ctcagttctg 1400

cttgaatacc tccatcgatg gggaactcac ttcctttgga aaaattctta 1450

tgtcaagctg aaattctcta atttttttctc atcacttccc caggagcagc 1500

cagaagacag gcagtagttt taatttcagg aacaggtgat ccactctgta 1550

aaacagcagg taaatttcac tcaaccccat gtgggaattg atctatatct 1600

ctacttccag ggaccatttg cccttcccaa atccctccag gccagaactg 1650

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ccccactcca gccctgggac aacttgagaa ttccccctga ggccagttct 1750

gtcatggatg ctgtcctgag aataacttgc tgtcccggtg tcacctgctt 1800

ccatctccca gcccaccagc cctctgccca cctcacatgc ctccccatgg 1850

attggggcct cccaggcccc ccaccttatg tcaacctgca cttcttgttc 1900

aaaaatcagg aaaagaaaag atttgaagac cccaagtctt gtcaataact 1950

tgctgtgtgg aagcagcggg ggaagaccta gaacccttc cccagcactt 2000

ggttttccaa catgatattt atgagtaatt tattttgata tgtacatctc 2050

ttatttttctt acattattta tgcccccaaa ttatatttat gtatgtaagt 2100

gaggtttgtt ttgtatatta aaatggagtt tgtttgt 2137

<210> 59
<211> 216
<212> PRT
<213> Homo Sapien

<400> 59

Met	Arg	Ser	Gly	Cys	Val	Val	Val	His	Val	Trp	Ile	Leu	Ala	Gly	
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Leu	Trp	Leu	Ala	Val	Ala	Gly	Arg	Pro	Leu	Ala	Phe	Ser	Asp	Ala	
				20					25						30
Gly	Pro	His	Val	His	Tyr	Gly	Trp	Gly	Asp	Pro	Ile	Arg	Leu	Arg	
				35					40						45
His	Leu	Tyr	Thr	Ser	Gly	Pro	His	Gly	Leu	Ser	Ser	Cys	Phe	Leu	
				50					55						60
Arg	Ile	Arg	Ala	Asp	Gly	Val	Val	Asp	Cys	Ala	Arg	Gly	Gln	Ser	
				65					70						75
Ala	His	Ser	Leu	Leu	Glu	Ile	Lys	Ala	Val	Ala	Leu	Arg	Thr	Val	
				80					85						90
Ala	Ile	Lys	Gly	Val	His	Ser	Val	Arg	Tyr	Leu	Cys	Met	Gly	Ala	
				95					100						105
Asp	Gly	Lys	Met	Gln	Gly	Leu	Leu	Gln	Tyr	Ser	Glu	Glu	Asp	Cys	
				110					115						120
Ala	Phe	Glu	Glu	Glu	Ile	Arg	Pro	Asp	Gly	Tyr	Asn	Val	Tyr	Arg	
				125					130						135
Ser	Glu	Lys	His	Arg	Leu	Pro	Val	Ser	Leu	Ser	Ser	Ala	Lys	Gln	
				140					145						150
Arg	Gln	Leu	Tyr	Lys	Asn	Arg	Gly	Phe	Leu	Pro	Leu	Ser	His	Phe	
				155					160						165
Leu	Pro	Met	Leu	Pro	Met	Val	Pro	Glu	Glu	Pro	Glu	Asp	Leu	Arg	
				170					175						180
Gly	His	Leu	Glu	Ser	Asp	Met	Phe	Ser	Ser	Pro	Leu	Glu	Thr	Asp	
				185					190						195
Ser	Met	Asp	Pro	Phe	Gly	Leu	Val	Thr	Gly	Leu	Glu	Ala	Val	Arg	
				200					205						210
Ser	Pro	Ser	Phe	Glu	Lys										
				215											

<210> 60
<211> 26
<212> DNA

<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 60
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<210> 61
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<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 61
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<210> 62
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 62
ccagtccggt gacaagccca aa 22

<210> 63
<211> 1295
<212> DNA
<213> Homo Sapien

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cccagaagtt caagggcccc cggcctcctg cgctcctgcc gccgggaccc 50

tcgacctcct cagagcagcc ggctgccgcc ccgggaagat ggcgaggagg 100

agccgccacc gcctcctcct gctgctgctg cgctacctgg tggtcgccct 150

gggctatcat aaggcctatg ggttttctgc cccaaaagac caacaagtag 200

tcacagcagt agagtaccaa gaggctattt tagcctgcaa aaccccaaag 250

aagactgttt cctccagatt agagtggaag aaactgggtc ggagtgtctc 300

ctttgtctac tatcaacaga ctcttcaagg tgattttaaa aatcgagctg 350

agatgataga tttcaatatc cggatcaaaa atgtgacaag aagtgatgcg 400

gggaaatatc gttgtgaagt tagtgcccca tctgagcaag gccaaaacct 450

ggaagaggat acagtcactc tggaagtatt agtggctcca gcagttccat 500

catgtgaagt accctcttct gctctgagtg gaactgtggt agagctacga 550

tgtcaagaca aagaagggaa tccagctcct gaatacacat ggtttaagga 600

tggcatccgt ttgctagaaa atcccagact tggctcccaa agcaccaaca 650

gctcatacac aatgaataca aaaactggaa ctctgcaatt taatactgtt 700

tccaaactgg acactggaga atattcctgt gaagcccgca attctgttgg 750

atatcgcagg tgtcctggga aacgaatgca agtagatgat ctcaacataa 800

gtggcatcat agcagccgta gtagttgtgg ccttagtgat ttccgtttgt 850

ggccttggtg tatgctatgc tcagaggaaa ggctactttt caaaagaaac 900

ctccttccag aagagtaatt cttcatctaa agccacgaca atgagtgaaa 950

atgtgcagtg gctcacgcct gtaatcccag cactttggaa ggccgcggcg 1000

ggcggatcac gaggtcagga gttctagacc agtctggcca atatggtgaa 1050

accccatctc tactaaaata caaaaattag ctgggcatgg tggcatgtgc 1100

ctgcagttcc agctgcttgg gagacaggag aatcacttga acccgggagg 1150

cggaggttgc agtgagctga gatcacgcca ctgcagtcca gcctgggtaa 1200

cagagcaaga ttccatctca aaaaataaaa taaataaata aataaatact 1250

ggtttttacc tgtagaattc ttacaataaa tatagcttga tattc 1295

<210> 64
<211> 312
<212> PRT
<213> Homo Sapien

<400> 64

Met	Ala	Arg	Arg	Ser	Arg	His	Arg	Leu	Leu	Leu	Leu	Leu	Leu	Arg	
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Tyr	Leu	Val	Val	Ala	Leu	Gly	Tyr	His	Lys	Ala	Tyr	Gly	Phe	Ser	
				20				25						30	
Ala	Pro	Lys	Asp	Gln	Gln	Val	Val	Thr	Ala	Val	Glu	Tyr	Gln	Glu	
				35				40						45	
Ala	Ile	Leu	Ala	Cys	Lys	Thr	Pro	Lys	Lys	Thr	Val	Ser	Ser	Arg	
				50				55						60	
Leu	Glu	Trp	Lys	Lys	Leu	Gly	Arg	Ser	Val	Ser	Phe	Val	Tyr	Tyr	
				65				70						75	
Gln	Gln	Thr	Leu	Gln	Gly	Asp	Phe	Lys	Asn	Arg	Ala	Glu	Met	Ile	
				80				85						90	
Asp	Phe	Asn	Ile	Arg	Ile	Lys	Asn	Val	Thr	Arg	Ser	Asp	Ala	Gly	
				95				100						105	
Lys	Tyr	Arg	Cys	Glu	Val	Ser	Ala	Pro	Ser	Glu	Gln	Gly	Gln	Asn	
				110				115						120	
Leu	Glu	Glu	Asp	Thr	Val	Thr	Leu	Glu	Val	Leu	Val	Ala	Pro	Ala	
				125				130						135	
Val	Pro	Ser	Cys	Glu	Val	Pro	Ser	Ser	Ala	Leu	Ser	Gly	Thr	Val	
				140				145						150	
Val	Glu	Leu	Arg	Cys	Gln	Asp	Lys	Glu	Gly	Asn	Pro	Ala	Pro	Glu	
				155				160						165	

Tyr Thr Trp Phe Lys Asp Gly Ile Arg Leu Leu Glu Asn Pro Arg
170 175 180

Leu Gly Ser Gln Ser Thr Asn Ser Ser Tyr Thr Met Asn Thr Lys
185 190 195

Thr Gly Thr Leu Gln Phe Asn Thr Val Ser Lys Leu Asp Thr Gly
200 205 210

Glu Tyr Ser Cys Glu Ala Arg Asn Ser Val Gly Tyr Arg Arg Cys
215 220 225

Pro Gly Lys Arg Met Gln Val Asp Asp Leu Asn Ile Ser Gly Ile
230 235 240

Ile Ala Ala Val Val Val Val Ala Leu Val Ile Ser Val Cys Gly
245 250 255

Leu Gly Val Cys Tyr Ala Gln Arg Lys Gly Tyr Phe Ser Lys Glu
260 265 270

Thr Ser Phe Gln Lys Ser Asn Ser Ser Ser Lys Ala Thr Thr Met
275 280 285

Ser Glu Asn Val Gln Trp Leu Thr Pro Val Ile Pro Ala Leu Trp
290 295 300

Lys Ala Ala Ala Gly Gly Ser Arg Gly Gln Glu Phe
305 310

<210> 65
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 65
atcgttgtga agttagtgcc cc 22

<210> 66
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 66
acctgcgata tccaacagaa ttg 23

<210> 67
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 67
ggaagaggat acagtcactc tggaagtatt agtggctcca gcagttcc 48

<210> 68
<211> 2639
<212> DNA
<213> Homo Sapien

<400> 68
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gaggagaaag agaaagaaga ggaagatgtt gggcaacatt tatttaacat 100

gctccacagc ccggaccctg gcatcatgct gctattcctg caaatactga 150

agaagcatgg gatttaaata ttttacttct aaataaatga attactcaat 200

ctcctatgac catctataca tactccacct tcaaaaagta catcaatatt 250

atatcattaa ggaaatagta accttctctt ctccaatatg catgacattt 300

ttggacaatg caattgtggc actggcactt atttcagtga agaaaaactt 350

tgtggttcta tggcattcat catttgacaa atgcaagcat cttccttatc 400

aatcagctcc tattgaactt actagcactg actgtggaat ccttaagggc 450

ccattacatt tctgaagaag aaagctaaga tgaaggacat gccactccga 500

attcatgtgc tacttggcct agctatcact acactagtac aagctgtaga 550

taaaaaagtg gattgtccac ggttatgtac gtgtgaaatc aggccttggt 600

ttacacccag atccatttat atggaagcat ctacagtgga ttgtaatgat 650

ttaggtcttt taactttccc agccagattg ccagctaaca cacagattct 700

tctcctacag actaacaata ttgcaaaaat tgaatactcc acagactttc 750

cagtaaacct tactggcctg gatttatctc aaaacaattt atcttcagtc 800

accaatatta atgtaaaaaa gatgcctcag ctcctttctg tgtacctaga 850

ggaaaacaaa cttactgaac tgcctgaaaa atgtctgtcc gaactgagca 900

acttacaaga actctatatt aatcacaact tgctttctac aatttcacct 950

ggagccttta ttggcctaca taatcttctt cgacttcatc tcaattcaaa 1000

tagattgcag atgatcaaca gtaagtggtt tgatgctctt ccaaatctag 1050

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tttaagcctc ttatcaatct tcgcagcctg gttatagctg gtataaacct 1150

cacagaaata ccagataacg ccttggttgg actggaaaac ttagaaagca 1200

tctcttttta cgataacagg cttattaaag taccccatgt tgctcttcaa 1250

aaagttgtaa atctcaaatt tttggatcta aataaaaatc ctattaatag 1300

aatacgaagg ggtgatttta gcaatatgct acacttaaaa gagttgggga 1350

taaataatat gcctgagctg atttccatcg atagtcttgc tgtggataac 1400

ctgccagatt taagaaaaat agaagctact aacaacccta gattgtctta 1450

cattcacccc aatgcatttt tcagactccc caagctggaa tcactcatgc 1500

tgaacagcaa tgctctcagt gccctgtacc atggtaccat tgagtctctg 1550

ccaaacctca aggaaatcag catacacagt aaccccatca ggtgtgactg 1600

tgtcatccgt tggatgaaca tgaacaaaac caacattcga ttcatggagc 1650

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acaccttctg gtcaaaaact cttgcctaat accctgacag acaagttcta 1900

tgtccattct gagggaacac tagatataaa tggcgtaact cccaaagaag 1950

ggggtttata tacttgtata gcaactaacc tagttggcgc tgacttgaag 2000

tctgttatga tcaaagtgga tggatctttt ccacaagata acaatggctc 2050

tttgaatatt aaaataagag atattcaggc caattcagtt ttggtgtcct 2100

ggaaagcaag ttctaaaatt ctcaaatcta gtgttaaatg gacagccttt 2150

gtcaagactg aaaattctca tgctgcgcaa agtgctcgaa taccatctga 2200

tgtcaaggta tataatctta ctcatctgaa tccatcaact gagtataaaa 2250

tttgtattga tattcccacc atctatcaga aaaacagaaa aaaatgtgta 2300

aatgtcacca ccaaaggttt gcaccctgat caaaaagagt atgaaaagaa 2350

taataccaca acacttatgg cctgtcttgg aggccttctg gggattattg 2400

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gtacatcact gaaagtaaaa gcaactgtta taggtttacc aacaaatatg 2600

tcctaaaaac caccaaggaa acctactcca aaaatgaac 2639

<210> 69
<211> 708
<212> PRT
<213> Homo Sapien

<400> 69

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Ile Thr Thr Leu Val Gln Ala Val Asp Lys Lys Val Asp Cys Pro
20 25 30

Arg Leu Cys Thr Cys Glu Ile Arg Pro Trp Phe Thr Pro Arg Ser

35 40 45

Ile Tyr Met Glu Ala Ser Thr Val Asp Cys Asn Asp Leu Gly Leu
50 55 60

Leu Thr Phe Pro Ala Arg Leu Pro Ala Asn Thr Gln Ile Leu Leu
65 70 75

Leu Gln Thr Asn Asn Ile Ala Lys Ile Glu Tyr Ser Thr Asp Phe
80 85 90

Pro Val Asn Leu Thr Gly Leu Asp Leu Ser Gln Asn Asn Leu Ser
95 100 105

Ser Val Thr Asn Ile Asn Val Lys Lys Met Pro Gln Leu Leu Ser
110 115 120

Val Tyr Leu Glu Glu Asn Lys Leu Thr Glu Leu Pro Glu Lys Cys
125 130 135

Leu Ser Glu Leu Ser Asn Leu Gln Glu Leu Tyr Ile Asn His Asn
140 145 150

Leu Leu Ser Thr Ile Ser Pro Gly Ala Phe Ile Gly Leu His Asn
155 160 165

Leu Leu Arg Leu His Leu Asn Ser Asn Arg Leu Gln Met Ile Asn
170 175 180

Ser Lys Trp Phe Asp Ala Leu Pro Asn Leu Glu Ile Leu Met Ile
185 190 195

Gly Glu Asn Pro Ile Ile Arg Ile Lys Asp Met Asn Phe Lys Pro
200 205 210

Leu Ile Asn Leu Arg Ser Leu Val Ile Ala Gly Ile Asn Leu Thr
215 220 225

Glu Ile Pro Asp Asn Ala Leu Val Gly Leu Glu Asn Leu Glu Ser
230 235 240

Ile Ser Phe Tyr Asp Asn Arg Leu Ile Lys Val Pro His Val Ala
245 250 255

Leu Gln Lys Val Val Asn Leu Lys Phe Leu Asp Leu Asn Lys Asn
260 265 270

Pro Ile Asn Arg Ile Arg Arg Gly Asp Phe Ser Asn Met Leu His
275 280 285

Leu Lys Glu Leu Gly Ile Asn Asn Met Pro Glu Leu Ile Ser Ile
290 295 300

Asp Ser Leu Ala Val Asp Asn Leu Pro Asp Leu Arg Lys Ile Glu
305 310 315

Ala Thr Asn Asn Pro Arg Leu Ser Tyr Ile His Pro Asn Ala Phe
320 325 330

Phe Arg Leu Pro Lys Leu Glu Ser Leu Met Leu Asn Ser Asn Ala
335 340 345

Leu Ser Ala Leu Tyr His Gly Thr Ile Glu Ser Leu Pro Asn Leu

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                350                 355                 360

Lys Glu Ile Ser Ile His Ser Asn Pro Ile Arg Cys Asp Cys Val
                365                 370                 375

Ile Arg Trp Met Asn Met Asn Lys Thr Asn Ile Arg Phe Met Glu
                380                 385                 390

Pro Asp Ser Leu Phe Cys Val Asp Pro Pro Glu Phe Gln Gly Gln
                395                 400                 405

Asn Val Arg Gln Val His Phe Arg Asp Met Met Glu Ile Cys Leu
                410                 415                 420

Pro Leu Ile Ala Pro Glu Ser Phe Pro Ser Asn Leu Asn Val Glu
                425                 430                 435

Ala Gly Ser Tyr Val Ser Phe His Cys Arg Ala Thr Ala Glu Pro
                440                 445                 450

Gln Pro Glu Ile Tyr Trp Ile Thr Pro Ser Gly Gln Lys Leu Leu
                455                 460                 465

Pro Asn Thr Leu Thr Asp Lys Phe Tyr Val His Ser Glu Gly Thr
                470                 475                 480

Leu Asp Ile Asn Gly Val Thr Pro Lys Glu Gly Gly Leu Tyr Thr
                485                 490                 495

Cys Ile Ala Thr Asn Leu Val Gly Ala Asp Leu Lys Ser Val Met
                500                 505                 510

Ile Lys Val Asp Gly Ser Phe Pro Gln Asp Asn Asn Gly Ser Leu
                515                 520                 525

Asn Ile Lys Ile Arg Asp Ile Gln Ala Asn Ser Val Leu Val Ser
                530                 535                 540

Trp Lys Ala Ser Ser Lys Ile Leu Lys Ser Ser Val Lys Trp Thr
                545                 550                 555

Ala Phe Val Lys Thr Glu Asn Ser His Ala Ala Gln Ser Ala Arg
                560                 565                 570

Ile Pro Ser Asp Val Lys Val Tyr Asn Leu Thr His Leu Asn Pro
                575                 580                 585

Ser Thr Glu Tyr Lys Ile Cys Ile Asp Ile Pro Thr Ile Tyr Gln
                590                 595                 600

Lys Asn Arg Lys Lys Cys Val Asn Val Thr Thr Lys Gly Leu His
                605                 610                 615

Pro Asp Gln Lys Glu Tyr Glu Lys Asn Asn Thr Thr Thr Leu Met
                620                 625                 630

Ala Cys Leu Gly Gly Leu Leu Gly Ile Ile Gly Val Ile Cys Leu
                635                 640                 645

Ile Ser Cys Leu Ser Pro Glu Met Asn Cys Asp Gly Gly His Ser
                650                 655                 660

Tyr Val Arg Asn Tyr Leu Gln Lys Pro Thr Phe Ala Leu Gly Glu
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665 670 675

Leu Tyr Pro Pro Leu Ile Asn Leu Trp Glu Ala Gly Lys Glu Lys
680 685 690

Ser Thr Ser Leu Lys Val Lys Ala Thr Val Ile Gly Leu Pro Thr
695 700 705

Asn Met Ser

<210> 70
<211> 1305
<212> DNA
<213> Homo Sapien

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tgtggacagg gctggaacct ttaccacgct tgttggagta gatgaggaat 150

gggctcgtga ttatgctgac attccagcat gaatctggta gacctgtggt 200

taacccgttc cctctccatg tgtctcctcc tacaaagttt tgttcttatg 250

atactgtgct ttcattctgc cagtatgtgt cccaagggct gtctttgttc 300

ttcctctggg ggtttaaatg tcacctgtag caatgcaaat ctcaaggaaa 350

tacctagaga tcttcctcct gaaacagtct tactgtatct ggactccaat 400

cagatcacat ctattcccaa tgaaattttt aaggacctcc atcaactgag 450

agttctcaac ctgtccaaaa atggcattga gtttatcgat gagcatgcct 500

tcaaaggagt agctgaaacc ttgcagactc tggacttgtc cgacaatcgg 550

attcaaagtg tgcacaaaaa tgccttcaat aacctgaagg ccagggccag 600

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gtgaggcaaa atcaggagga tgcccggaga cacctcgaat acttgaaatc 900

cctgccaagc aggcagaaga aagcagatga acctgatgat attagcactg 950

tggtatagtg tccaaactga ctgtcattga gaaagaaaga aagtagtttg 1000

cgattgcagt agaaataagt ggtttacttc tcccatccat tgtaaacatt 1050

tgaaactttg tatttcagtt ttttttgaat tatgccactg ctgaactttt 1100

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caaataaaag cttaactttg aaccatggga aaaaaaaaaa aaaaaaaaaa 1300

aaaca 1305

<210> 71
<211> 259
<212> PRT
<213> Homo Sapien

<400> 71

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             20                  25                  30

Ala Ser Met Cys Pro Lys Gly Cys Leu Cys Ser Ser Ser Gly Gly
             35                  40                  45

Leu Asn Val Thr Cys Ser Asn Ala Asn Leu Lys Glu Ile Pro Arg
             50                  55                  60

Asp Leu Pro Pro Glu Thr Val Leu Leu Tyr Leu Asp Ser Asn Gln
             65                  70                  75

Ile Thr Ser Ile Pro Asn Glu Ile Phe Lys Asp Leu His Gln Leu
             80                  85                  90

Arg Val Leu Asn Leu Ser Lys Asn Gly Ile Glu Phe Ile Asp Glu
             95                 100                 105

His Ala Phe Lys Gly Val Ala Glu Thr Leu Gln Thr Leu Asp Leu
            110                 115                 120

Ser Asp Asn Arg Ile Gln Ser Val His Lys Asn Ala Phe Asn Asn
            125                 130                 135

Leu Lys Ala Arg Ala Arg Ile Ala Asn Asn Pro Trp His Cys Asp
            140                 145                 150

Cys Thr Leu Gln Gln Val Leu Arg Ser Met Ala Ser Asn His Glu
            155                 160                 165

Thr Ala His Asn Val Ile Cys Lys Thr Ser Val Leu Asp Glu His
            170                 175                 180

Ala Gly Arg Pro Phe Leu Asn Ala Ala Asn Asp Ala Asp Leu Cys
            185                 190                 195

Asn Leu Pro Lys Lys Thr Thr Asp Tyr Ala Met Leu Val Thr Met
            200                 205                 210

Phe Gly Trp Phe Thr Met Val Ile Ser Tyr Val Val Tyr Tyr Val
            215                 220                 225

Arg Gln Asn Gln Glu Asp Ala Arg Arg His Leu Glu Tyr Leu Lys
            230                 235                 240

Ser Leu Pro Ser Arg Gln Lys Lys Ala Asp Glu Pro Asp Asp Ile
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245 250 255

Ser Thr Val Val

<210> 72
<211> 2290
<212> DNA
<213> Homo Sapien

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cgggctgccc gccccgctgc gagtgctccg cccaggaccg cgctgtgctg 200

tgccaccgca agtgctttgt ggcagtcccc gagggcatcc ccaccgagac 250

gcgcctgctg gacctaggca agaaccgcat caaaacgctc aaccaggacg 300

agttcgccag cttcccgcac ctggaggagc tggagctcaa cgagaacatc 350

gtgagcgccg tggagcccgg cgccttcaac aacctcttca acctccggac 400

gctgggtctc cgcagcaacc gcctgaagct catcccgcta ggcgtcttca 450

ctggcctcag caacctgacc aagcaggaca tcagcgagaa caagatcgtt 500

atcctactgg actacatgtt tcaggacctg tacaacctca agtcactgga 550

ggttggcgac aatgacctcg tctacatctc tcaccgcgcc ttcagcggcc 600

tcaacagcct ggagcagctg acgctggaga aatgcaacct gacctccatc 650

cccaccgagg cgctgtccca cctgcacggc ctcatcgtcc tgaggctccg 700

gcacctcaac atcaatgcca tccgggacta ctccttcaag aggctgtacc 750

gactcaaggt cttggagatc tcccactggc cctacttgga caccatgaca 800

cccaactgcc tctacggcct caacctgacg tccctgtcca tcacacactg 850

caatctgacc gctgtgccct acctggccgt ccgccaccta gtctatctcc 900

gcttcctcaa cctctcctac aaccccatca gcaccattga gggctccatg 950

ttgcatgagc tgctccggct gcaggagatc cagctggtgg gcgggcagct 1000

ggccgtggtg gagccctatg ccttccgcgg cctcaactac ctgcgcgtgc 1050

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cgactgtcgg ctcctgtggg tgttccggcg ccgctggcgg ctcaacttca 1200

accggcagca gcccacgtgc gccacgcccg agtttgtcca gggcaaggag 1250

ttcaaggact tccctgatgt gctactgccc aactacttca cctgccgccg 1300

cgcccgcatc cgggaccgca aggcccagca ggtgtttgtg gacgagggcc 1350

acacggtgca gtttgtgtgc cgggccgatg gcgacccgcc gcccgccatc 1400

ctctggctct caccccgaaa gcacctggtc tcagccaaga gcaatgggcg 1450

gctcacagtc ttccctgatg gcacgctgga ggtgcgctac gcccaggtac 1500

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tccatgcccg cccacctgca tgtgcgcagc tactcgcccg actggcccca 1600

tcagcccaac aagaccttcg ctttcatctc caaccagccg ggcgagggag 1650

aggccaacag cacccgcgcc actgtgcctt tccccttcga catcaagacc 1700

ctcatcatcg ccaccaccat gggcttcatc tctttcctgg gcgtcgtcct 1750

cttctgcctg gtgctgctgt ttctctggag ccggggcaag ggcaacacaa 1800

agcacaacat cgagatcgag tatgtgcccc gaaagtcgga cgcaggcatc 1850

agctccgccg acgcgccccg caagttcaac atgaagatga tatgaggccg 1900

gggcgggggg cagggacccc cgggcggccg ggcaggggaa ggggcctggt 1950

cgccacctgc tcactctcca gtccttccca cctcctccct acccttctac 2000

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ggaccccacc tacacagggg cattgacaga ctggagttga aagccgacga 2150

accgacacgc ggcagagtca ataattcaat aaaaaagtta cgaactttct 2200

ctgtaacttg ggtttcaata attatggatt tttatgaaaa cttgaaataa 2250

taaaaagaga aaaaaactaa aaaaaaaaaa aaaaaaaaaa 2290

<210> 73
<211> 620
<212> PRT
<213> Homo Sapien

<400> 73

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Pro	Ser	Pro	Leu	Leu	Ala	Cys	Trp	Gln	Pro	Ile	Leu	Leu	Leu	Val	
				20				25						30	
Leu	Gly	Ser	Val	Leu	Ser	Gly	Ser	Ala	Thr	Gly	Cys	Pro	Pro	Arg	
				35				40						45	
Cys	Glu	Cys	Ser	Ala	Gln	Asp	Arg	Ala	Val	Leu	Cys	His	Arg	Lys	
				50				55						60	
Cys	Phe	Val	Ala	Val	Pro	Glu	Gly	Ile	Pro	Thr	Glu	Thr	Arg	Leu	
				65				70						75	
Leu	Asp	Leu	Gly	Lys	Asn	Arg	Ile	Lys	Thr	Leu	Asn	Gln	Asp	Glu	
				80				85						90	

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Phe Ala Ser Phe Pro His Leu Glu Glu Leu Glu Leu Asn Glu Asn
 95                 100                 105

Ile Val Ser Ala Val Glu Pro Gly Ala Phe Asn Asn Leu Phe Asn
110                 115                 120

Leu Arg Thr Leu Gly Leu Arg Ser Asn Arg Leu Lys Leu Ile Pro
125                 130                 135

Leu Gly Val Phe Thr Gly Leu Ser Asn Leu Thr Lys Gln Asp Ile
140                 145                 150

Ser Glu Asn Lys Ile Val Ile Leu Leu Asp Tyr Met Phe Gln Asp
155                 160                 165

Leu Tyr Asn Leu Lys Ser Leu Glu Val Gly Asp Asn Asp Leu Val
170                 175                 180

Tyr Ile Ser His Arg Ala Phe Ser Gly Leu Asn Ser Leu Glu Gln
185                 190                 195

Leu Thr Leu Glu Lys Cys Asn Leu Thr Ser Ile Pro Thr Glu Ala
200                 205                 210

Leu Ser His Leu His Gly Leu Ile Val Leu Arg Leu Arg His Leu
215                 220                 225

Asn Ile Asn Ala Ile Arg Asp Tyr Ser Phe Lys Arg Leu Tyr Arg
230                 235                 240

Leu Lys Val Leu Glu Ile Ser His Trp Pro Tyr Leu Asp Thr Met
245                 250                 255

Thr Pro Asn Cys Leu Tyr Gly Leu Asn Leu Thr Ser Leu Ser Ile
260                 265                 270

Thr His Cys Asn Leu Thr Ala Val Pro Tyr Leu Ala Val Arg His
275                 280                 285

Leu Val Tyr Leu Arg Phe Leu Asn Leu Ser Tyr Asn Pro Ile Ser
290                 295                 300

Thr Ile Glu Gly Ser Met Leu His Glu Leu Leu Arg Leu Gln Glu
305                 310                 315

Ile Gln Leu Val Gly Gly Gln Leu Ala Val Val Glu Pro Tyr Ala
320                 325                 330

Phe Arg Gly Leu Asn Tyr Leu Arg Val Leu Asn Val Ser Gly Asn
335                 340                 345

Gln Leu Thr Thr Leu Glu Glu Ser Val Phe His Ser Val Gly Asn
350                 355                 360

Leu Glu Thr Leu Ile Leu Asp Ser Asn Pro Leu Ala Cys Asp Cys
365                 370                 375

Arg Leu Leu Trp Val Phe Arg Arg Arg Trp Arg Leu Asn Phe Asn
380                 385                 390

Arg Gln Gln Pro Thr Cys Ala Thr Pro Glu Phe Val Gln Gly Lys
395                 400                 405
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Glu Phe Lys Asp Phe Pro Asp Val Leu Leu Pro Asn Tyr Phe Thr
410 415 420

Cys Arg Arg Ala Arg Ile Arg Asp Arg Lys Ala Gln Gln Val Phe
425 430 435

Val Asp Glu Gly His Thr Val Gln Phe Val Cys Arg Ala Asp Gly
440 445 450

Asp Pro Pro Pro Ala Ile Leu Trp Leu Ser Pro Arg Lys His Leu
455 460 465

Val Ser Ala Lys Ser Asn Gly Arg Leu Thr Val Phe Pro Asp Gly
470 475 480

Thr Leu Glu Val Arg Tyr Ala Gln Val Gln Asp Asn Gly Thr Tyr
485 490 495

Leu Cys Ile Ala Ala Asn Ala Gly Gly Asn Asp Ser Met Pro Ala
500 505 510

His Leu His Val Arg Ser Tyr Ser Pro Asp Trp Pro His Gln Pro
515 520 525

Asn Lys Thr Phe Ala Phe Ile Ser Asn Gln Pro Gly Glu Gly Glu
530 535 540

Ala Asn Ser Thr Arg Ala Thr Val Pro Phe Pro Phe Asp Ile Lys
545 550 555

Thr Leu Ile Ile Ala Thr Thr Met Gly Phe Ile Ser Phe Leu Gly
560 565 570

Val Val Leu Phe Cys Leu Val Leu Leu Phe Leu Trp Ser Arg Gly
575 580 585

Lys Gly Asn Thr Lys His Asn Ile Glu Ile Glu Tyr Val Pro Arg
590 595 600

Lys Ser Asp Ala Gly Ile Ser Ser Ala Asp Ala Pro Arg Lys Phe
605 610 615

Asn Met Lys Met Ile
620

<210> 74
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 74
tcacctggag cctttattgg cc 22

<210> 75
<211> 23
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 75
ataccagcta taaccaggct gcg 23

<210> 76
<211> 52
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 76
caacagtaag tggtttgatg ctcttccaaa tctagagatt ctgatgattg 50

gg 52

<210> 77
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 77
ccatgtgtct cctcctacaa ag 22

<210> 78
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 78
gggaatagat gtgatctgat tgg 23

<210> 79
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 79
cacctgtagc aatgcaaatc tcaaggaaat acctagagat cttcctcctg 50

<210> 80
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 80
agcaaccgcc tgaagctcat cc 22

<210> 81

<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 81
aaggcgcggt gaaagatgta gacg 24

<210> 82
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 82
gactacatgt ttcaggacct gtacaacctc aagtcactgg aggttggcga 50

<210> 83
<211> 1685
<212> DNA
<213> Homo Sapien

<400> 83
cccacgcgtc cgcacctcgg ccccgggctc cgaagcggct cgggggcgcc 50

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attcaggctc gccagcgccc agccagggag ccggccggga agcgcgatgg 150

gggccccagc cgcctcgctc ctgctcctgc tcctgctgtt cgcctgctgc 200

tgggcgcccg gcggggccaa cctctcccag gacgacagcc agccctggac 250

atctgatgaa acagtggtgg ctggtggcac cgtggtgctc aagtgccaag 300

tgaaagatca cgaggactca tccctgcaat ggtctaaccc tgctcagcag 350

actctctact ttggggagaa gagagccctt cgagataatc gaattcagct 400

ggttacctct acgccccacg agctcagcat cagcatcagc aatgtggccc 450

tggcagacga gggcgagtac acctgctcaa tcttcactat gcctgtgcga 500

actgccaagt ccctcgtcac tgtgctagga attccacaga agcccatcat 550

cactggttat aaatcttcat tacgggaaaa agacacagcc accctaaact 600

gtcagtcttc tgggagcaag cctgcagccc ggctcacctg gagaaagggt 650

gaccaagaac tccacggaga accaacccgc atacaggaag atcccaatgg 700

taaaaccttc actgtcagca gctcggtgac attccaggtt acccgggagg 750

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ctggggtgag aaaagcaaaa aacaaacaaa aaaca 1685

<210> 84
<211> 398
<212> PRT
<213> Homo Sapien

<400> 84

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Met Gly Ala Pro Ala Ala Ser Leu Leu Leu Leu Leu Leu Leu Phe
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Ala Cys Cys Trp Ala Pro Gly Gly Ala Asn Leu Ser Gln Asp Asp
             20                  25                  30

Ser Gln Pro Trp Thr Ser Asp Glu Thr Val Val Ala Gly Gly Thr
             35                  40                  45

Val Val Leu Lys Cys Gln Val Lys Asp His Glu Asp Ser Ser Leu
             50                  55                  60

Gln Trp Ser Asn Pro Ala Gln Gln Thr Leu Tyr Phe Gly Glu Lys
             65                  70                  75

Arg Ala Leu Arg Asp Asn Arg Ile Gln Leu Val Thr Ser Thr Pro
             80                  85                  90

His Glu Leu Ser Ile Ser Ile Ser Asn Val Ala Leu Ala Asp Glu
             95                 100                 105

Gly Glu Tyr Thr Cys Ser Ile Phe Thr Met Pro Val Arg Thr Ala
            110                 115                 120

Lys Ser Leu Val Thr Val Leu Gly Ile Pro Gln Lys Pro Ile Ile
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125 130 135

Thr Gly Tyr Lys Ser Ser Leu Arg Glu Lys Asp Thr Ala Thr Leu
140 145 150

Asn Cys Gln Ser Ser Gly Ser Lys Pro Ala Ala Arg Leu Thr Trp
155 160 165

Arg Lys Gly Asp Gln Glu Leu His Gly Glu Pro Thr Arg Ile Gln
170 175 180

Glu Asp Pro Asn Gly Lys Thr Phe Thr Val Ser Ser Ser Val Thr
185 190 195

Phe Gln Val Thr Arg Glu Asp Asp Gly Ala Ser Ile Val Cys Ser
200 205 210

Val Asn His Glu Ser Leu Lys Gly Ala Asp Arg Ser Thr Ser Gln
215 220 225

Arg Ile Glu Val Leu Tyr Thr Pro Thr Ala Met Ile Arg Pro Asp
230 235 240

Pro Pro His Pro Arg Glu Gly Gln Lys Leu Leu Leu His Cys Glu
245 250 255

Gly Arg Gly Asn Pro Val Pro Gln Gln Tyr Leu Trp Glu Lys Glu
260 265 270

Gly Ser Val Pro Pro Leu Lys Met Thr Gln Glu Ser Ala Leu Ile
275 280 285

Phe Pro Phe Leu Asn Lys Ser Asp Ser Gly Thr Tyr Gly Cys Thr
290 295 300

Ala Thr Ser Asn Met Gly Ser Tyr Lys Ala Tyr Tyr Thr Leu Asn
305 310 315

Val Asn Asp Pro Ser Pro Val Pro Ser Ser Ser Ser Thr Tyr His
320 325 330

Ala Ile Ile Gly Gly Ile Val Ala Phe Ile Val Phe Leu Leu Leu
335 340 345

Ile Met Leu Ile Phe Leu Gly His Tyr Leu Ile Arg His Lys Gly
350 355 360

Thr Tyr Leu Thr His Glu Ala Lys Gly Ser Asp Asp Ala Pro Asp
365 370 375

Ala Asp Thr Ala Ile Ile Asn Ala Glu Gly Gly Gln Ser Gly Gly
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Asp Asp Lys Lys Glu Tyr Phe Ile
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<210> 85
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 85
gctaggaatt ccacagaagc cc 22

<210> 86
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 86
aacctggaat gtcaccgagc tg 22

<210> 87
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 87
cctagcacag tgacgaggga cttggc 26

<210> 88
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 88
aagacacagc caccctaaac tgtcagtctt ctgggagcaa gcctgcagcc 50

<210> 89
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Sequence

<400> 89
gccctggcag acgagggcga gtacacctgc tcaatcttca ctatgcctgt 50

<210> 90
<211> 2755
<212> DNA
<213> Homo Sapien

<400> 90
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gggcagttgc acgaaggcat gaatgtattg taaataagta actttgactt 2750

ctgac 2755

<210> 91
<211> 696
<212> PRT
<213> Homo Sapien

<400> 91

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				20				25						30	
Cys	Asn	Glu	Ile	Glu	Gly	Asp	Leu	His	Val	Asp	Cys	Glu	Lys	Lys	
				35				40						45	
Gly	Phe	Thr	Ser	Leu	Gln	Arg	Phe	Thr	Ala	Pro	Thr	Ser	Gln	Phe	
				50				55						60	
Tyr	His	Leu	Phe	Leu	His	Gly	Asn	Ser	Leu	Thr	Arg	Leu	Phe	Pro	
				65				70						75	
Asn	Glu	Phe	Ala	Asn	Phe	Tyr	Asn	Ala	Val	Ser	Leu	His	Met	Glu	
				80				85						90	

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Asn Asn Gly Leu His Glu Ile Val Pro Gly Ala Phe Leu Gly Leu
                 95                  100                 105

Gln Leu Val Lys Arg Leu His Ile Asn Asn Asn Lys Ile Lys Ser
                110                 115                 120

Phe Arg Lys Gln Thr Phe Leu Gly Leu Asp Asp Leu Glu Tyr Leu
                125                 130                 135

Gln Ala Asp Phe Asn Leu Leu Arg Asp Ile Asp Pro Gly Ala Phe
                140                 145                 150

Gln Asp Leu Asn Lys Leu Glu Val Leu Ile Leu Asn Asp Asn Leu
                155                 160                 165

Ile Ser Thr Leu Pro Ala Asn Val Phe Gln Tyr Val Pro Ile Thr
                170                 175                 180

His Leu Asp Leu Arg Gly Asn Arg Leu Lys Thr Leu Pro Tyr Glu
                185                 190                 195

Glu Val Leu Glu Gln Ile Pro Gly Ile Ala Glu Ile Leu Leu Glu
                200                 205                 210

Asp Asn Pro Trp Asp Cys Thr Cys Asp Leu Leu Ser Leu Lys Glu
                215                 220                 225

Trp Leu Glu Asn Ile Pro Lys Asn Ala Leu Ile Gly Arg Val Val
                230                 235                 240

Cys Glu Ala Pro Thr Arg Leu Gln Gly Lys Asp Leu Asn Glu Thr
                245                 250                 255

Thr Glu Gln Asp Leu Cys Pro Leu Lys Asn Arg Val Asp Ser Ser
                260                 265                 270

Leu Pro Ala Pro Pro Ala Gln Glu Glu Thr Phe Ala Pro Gly Pro
                275                 280                 285

Leu Pro Thr Pro Phe Lys Thr Asn Gly Gln Glu Asp His Ala Thr
                290                 295                 300

Pro Gly Ser Ala Pro Asn Gly Gly Thr Lys Ile Pro Gly Asn Trp
                305                 310                 315

Gln Ile Lys Ile Arg Pro Thr Ala Ala Ile Ala Thr Gly Ser Ser
                320                 325                 330

Arg Asn Lys Pro Leu Ala Asn Ser Leu Pro Cys Pro Gly Gly Cys
                335                 340                 345

Ser Cys Asp His Ile Pro Gly Ser Gly Leu Lys Met Asn Cys Asn
                350                 355                 360

Asn Arg Asn Val Ser Ser Leu Ala Asp Leu Lys Pro Lys Leu Ser
                365                 370                 375

Asn Val Gln Glu Leu Phe Leu Arg Asp Asn Lys Ile His Ser Ile
                380                 385                 390

Arg Lys Ser His Phe Val Asp Tyr Lys Asn Leu Ile Leu Leu Asp
                395                 400                 405
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Leu Gly Asn Asn Asn Ile Ala Thr Val Glu Asn Asn Thr Phe Lys
                410                 415                 420

Asn Leu Leu Asp Leu Arg Trp Leu Tyr Met Asp Ser Asn Tyr Leu
                425                 430                 435

Asp Thr Leu Ser Arg Glu Lys Phe Ala Gly Leu Gln Asn Leu Glu
                440                 445                 450

Tyr Leu Asn Val Glu Tyr Asn Ala Ile Gln Leu Ile Leu Pro Gly
                455                 460                 465

Thr Phe Asn Ala Met Pro Lys Leu Arg Ile Leu Ile Leu Asn Asn
                470                 475                 480

Asn Leu Leu Arg Ser Leu Pro Val Asp Val Phe Ala Gly Val Ser
                485                 490                 495

Leu Ser Lys Leu Ser Leu His Asn Asn Tyr Phe Met Tyr Leu Pro
                500                 505                 510

Val Ala Gly Val Leu Asp Gln Leu Thr Ser Ile Ile Gln Ile Asp
                515                 520                 525

Leu His Gly Asn Pro Trp Glu Cys Ser Cys Thr Ile Val Pro Phe
                530                 535                 540

Lys Gln Trp Ala Glu Arg Leu Gly Ser Glu Val Leu Met Ser Asp
                545                 550                 555

Leu Lys Cys Glu Thr Pro Val Asn Phe Phe Arg Lys Asp Phe Met
                560                 565                 570

Leu Leu Ser Asn Asp Glu Ile Cys Pro Gln Leu Tyr Ala Arg Ile
                575                 580                 585

Ser Pro Thr Leu Thr Ser His Ser Lys Asn Ser Thr Gly Leu Ala
                590                 595                 600

Glu Thr Gly Thr His Ser Asn Ser Tyr Leu Asp Thr Ser Arg Val
                605                 610                 615

Ser Ile Ser Val Leu Val Pro Gly Leu Leu Leu Val Phe Val Thr
                620                 625                 630

Ser Ala Phe Thr Val Val Gly Met Leu Val Phe Ile Leu Arg Asn
                635                 640                 645

Arg Lys Arg Ser Lys Arg Arg Asp Ala Asn Ser Ser Ala Ser Glu
                650                 655                 660

Ile Asn Ser Leu Gln Thr Val Cys Asp Ser Ser Tyr Trp His Asn
                665                 670                 675

Gly Pro Tyr Asn Ala Asp Gly Ala His Arg Val Tyr Asp Cys Gly
                680                 685                 690

Ser His Ser Leu Ser Asp
                695
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<210> 92
<211> 22

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 92
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<210> 93
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 93
attgttgtgc aggctgagtt taag 24

<210> 94
<211> 45
<212> DNA
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<220>
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<400> 94
ggtggctata catggatagc aattacctgg acacgctgtc ccggg 45

<210> 95
<211> 2226
<212> DNA
<213> Homo Sapien

<400> 95
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ataactcagg gctgcaccgg gcctggcagc gctccgcaca catttcctgt 100

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<210> 96
<211> 490
<212> PRT
<213> Homo Sapien

<400> 96

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             20                  25                  30

Cys Ser Ala Ser Gly Ala Cys Tyr Ser Leu His His Ala Thr Met
             35                  40                  45

Lys Arg Gln Ala Ala Glu Glu Ala Cys Ile Leu Arg Gly Gly Ala
             50                  55                  60

Leu Ser Thr Val Arg Ala Gly Ala Glu Leu Arg Ala Val Leu Ala
             65                  70                  75

Leu Leu Arg Ala Gly Pro Gly Pro Gly Gly Gly Ser Lys Asp Leu
             80                  85                  90

Leu Phe Trp Val Ala Leu Glu Arg Arg Arg Ser His Cys Thr Leu
             95                 100                 105

Glu Asn Glu Pro Leu Arg Gly Phe Ser Trp Leu Ser Ser Asp Pro
            110                 115                 120

Gly Gly Leu Glu Ser Asp Thr Leu Gln Trp Val Glu Glu Pro Gln
            125                 130                 135

Arg Ser Cys Thr Ala Arg Arg Cys Ala Val Leu Gln Ala Thr Gly
            140                 145                 150

Gly Val Glu Pro Ala Gly Trp Lys Glu Met Arg Cys His Leu Arg
            155                 160                 165

Ala Asn Gly Tyr Leu Cys Lys Tyr Gln Phe Glu Val Leu Cys Pro
            170                 175                 180

Ala Pro Arg Pro Gly Ala Ala Ser Asn Leu Ser Tyr Arg Ala Pro
            185                 190                 195

Phe Gln Leu His Ser Ala Ala Leu Asp Phe Ser Pro Pro Gly Thr
            200                 205                 210

Glu Val Ser Ala Leu Cys Arg Gly Gln Leu Pro Ile Ser Val Thr
            215                 220                 225

Cys Ile Ala Asp Glu Ile Gly Ala Arg Trp Asp Lys Leu Ser Gly
            230                 235                 240

Asp Val Leu Cys Pro Cys Pro Gly Arg Tyr Leu Arg Ala Gly Lys
            245                 250                 255

Cys Ala Glu Leu Pro Asn Cys Leu Asp Asp Leu Gly Gly Phe Ala
            260                 265                 270

Cys Glu Cys Ala Thr Gly Phe Glu Leu Gly Lys Asp Gly Arg Ser
            275                 280                 285
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Cys Val Thr Ser Gly Glu Gly Gln Pro Thr Leu Gly Gly Thr Gly
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Val Pro Thr Arg Arg Pro Pro Ala Thr Ala Thr Ser Pro Val Pro
                305                 310                 315

Gln Arg Thr Trp Pro Ile Arg Val Asp Glu Lys Leu Gly Glu Thr
                320                 325                 330

Pro Leu Val Pro Glu Gln Asp Asn Ser Val Thr Ser Ile Pro Glu
                335                 340                 345

Ile Pro Arg Trp Gly Ser Gln Ser Thr Met Ser Thr Leu Gln Met
                350                 355                 360

Ser Leu Gln Ala Glu Ser Lys Ala Thr Ile Thr Pro Ser Gly Ser
                365                 370                 375

Val Ile Ser Lys Phe Asn Ser Thr Thr Ser Ser Ala Thr Pro Gln
                380                 385                 390

Ala Phe Asp Ser Ser Ser Ala Val Val Phe Ile Phe Val Ser Thr
                395                 400                 405

Ala Val Val Val Leu Val Ile Leu Thr Met Thr Val Leu Gly Leu
                410                 415                 420

Val Lys Leu Cys Phe His Glu Ser Pro Ser Ser Gln Pro Arg Lys
                425                 430                 435

Glu Ser Met Gly Pro Pro Gly Leu Glu Ser Asp Pro Glu Pro Ala
                440                 445                 450

Ala Leu Gly Ser Ser Ser Ala His Cys Thr Asn Asn Gly Val Lys
                455                 460                 465

Val Gly Asp Cys Asp Leu Arg Asp Arg Ala Glu Gly Ala Leu Leu
                470                 475                 480

Ala Glu Ser Pro Leu Gly Ser Ser Asp Ala
                485                 490

<210> 97
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 97
 tggaaggaga tgcgatgcca cctg 24

<210> 98
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 98
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tgaccagtgg ggaaggacag 20

<210> 99
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 99
acagagcaga gggtgccttg 20

<210> 100
<211> 24
<212> DNA
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<220>
<223> Synthetic Oligonucleotide Probe

<400> 100
tcagggacaa gtggtgtctc tccc 24

<210> 101
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 101
tcagggaagg agtgtgcagt tctg 24

<210> 102
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 102
acagctcccg atctcagtta cttgcatcgc ggacgaaatc ggcgctcgct 50

<210> 103
<211> 2026
<212> DNA
<213> Homo Sapien

<400> 103
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ggggaaacta agcgtcgagt cagacggcac cataatcgcc tttaaaagtg 100

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cggtgcgcgc gtgagaggga gcgcgcgggc agccgagcgc cggtgtgagc 200

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gtaaaaggat attttagaat tgagttgtgt gaagatgtca aaaaaagatt 1900

ttagaagtgc aatatttata gtgttatttg tttcaccttc aagcctttgc 1950

cctgaggtgt tacaatcttg tcttgcgttt tctaaatcaa tgcttaataa 2000

aatattttta aaggaaaaaa aaaaaa 2026

<210> 104
<211> 415
<212> PRT
<213> Homo Sapien

<400> 104

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             20                  25                  30

Phe Thr Cys Gly Gly Ile Leu Thr Gly Glu Ser Gly Phe Ile Gly
             35                  40                  45

Ser Glu Gly Phe Pro Gly Val Tyr Pro Pro Asn Ser Lys Cys Thr
             50                  55                  60

Trp Lys Ile Thr Val Pro Glu Gly Lys Val Val Val Leu Asn Phe
             65                  70                  75

Arg Phe Ile Asp Leu Glu Ser Asp Asn Leu Cys Arg Tyr Asp Phe
             80                  85                  90

Val Asp Val Tyr Asn Gly His Ala Asn Gly Gln Arg Ile Gly Arg
             95                 100                 105

Phe Cys Gly Thr Phe Arg Pro Gly Ala Leu Val Ser Ser Gly Asn
            110                 115                 120

Lys Met Met Val Gln Met Ile Ser Asp Ala Asn Thr Ala Gly Asn
            125                 130                 135

Gly Phe Met Ala Met Phe Ser Ala Ala Glu Pro Asn Glu Arg Gly
            140                 145                 150

Asp Gln Tyr Cys Gly Gly Leu Leu Asp Arg Pro Ser Gly Ser Phe
            155                 160                 165

Lys Thr Pro Asn Trp Pro Asp Arg Asp Tyr Pro Ala Gly Val Thr
            170                 175                 180

Cys Val Trp His Ile Val Ala Pro Lys Asn Gln Leu Ile Glu Leu
            185                 190                 195

Lys Phe Glu Lys Phe Asp Val Glu Arg Asp Asn Tyr Cys Arg Tyr
            200                 205                 210

Asp Tyr Val Ala Val Phe Asn Gly Gly Glu Val Asn Asp Ala Arg
            215                 220                 225

Arg Ile Gly Lys Tyr Cys Gly Asp Ser Pro Pro Ala Pro Ile Val
            230                 235                 240

Ser Glu Arg Asn Glu Leu Leu Ile Gln Phe Leu Ser Asp Leu Ser
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245 250 255

Leu Thr Ala Asp Gly Phe Ile Gly His Tyr Ile Phe Arg Pro Lys
260 265 270

Lys Leu Pro Thr Thr Thr Glu Gln Pro Val Thr Thr Thr Phe Pro
275 280 285

Val Thr Thr Gly Leu Lys Pro Thr Val Ala Leu Cys Gln Gln Lys
290 295 300

Cys Arg Arg Thr Gly Thr Leu Glu Gly Asn Tyr Cys Ser Ser Asp
305 310 315

Phe Val Leu Ala Gly Thr Val Ile Thr Thr Ile Thr Arg Asp Gly
320 325 330

Ser Leu His Ala Thr Val Ser Ile Ile Asn Ile Tyr Lys Glu Gly
335 340 345

Asn Leu Ala Ile Gln Gln Ala Gly Lys Asn Met Ser Ala Arg Leu
350 355 360

Thr Val Val Cys Lys Gln Cys Pro Leu Leu Arg Arg Gly Leu Asn
365 370 375

Tyr Ile Ile Met Gly Gln Val Gly Glu Asp Gly Arg Gly Lys Ile
380 385 390

Met Pro Asn Ser Phe Ile Met Met Phe Lys Thr Lys Asn Gln Lys
395 400 405

Leu Leu Asp Ala Leu Lys Asn Lys Gln Cys
410 415

<210> 105
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 105
ccgattcata gacctcgaga gt 22

<210> 106
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 106
gtcaaggagt cctccacaat ac 22

<210> 107
<211> 45
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 107
gtgtacaatg gccatgccaa tggccagcgc attggccgct tctgt 45

<210> 108
<211> 1838
<212> DNA
<213> Homo Sapien

<400> 108
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ggtcttggaa agttaaaaaa aaaaaaaaaa aaaaaaaa 1838

<210> 109
<211> 420
<212> PRT
<213> Homo Sapien

<400> 109

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				20					25						30		
Pro	Ser	Pro	Pro	Pro	Gln	Ser	Ser	Pro	Pro	Pro	Gln	Pro	His	Pro			
				35					40						45		
Cys	His	Thr	Cys	Arg	Gly	Leu	Val	Asp	Ser	Phe	Asn	Lys	Gly	Leu			
				50					55						60		
Glu	Arg	Thr	Ile	Arg	Asp	Asn	Phe	Gly	Gly	Gly	Asn	Thr	Ala	Trp			
				65					70						75		
Glu	Glu	Glu	Asn	Leu	Ser	Lys	Tyr	Lys	Asp	Ser	Glu	Thr	Arg	Leu			
				80					85						90		
Val	Glu	Val	Leu	Glu	Gly	Val	Cys	Ser	Lys	Ser	Asp	Phe	Glu	Cys			
				95					100						105		
His	Arg	Leu	Leu	Glu	Leu	Ser	Glu	Glu	Leu	Val	Glu	Ser	Trp	Trp			
				110					115						120		
Phe	His	Lys	Gln	Gln	Glu	Ala	Pro	Asp	Leu	Phe	Gln	Trp	Leu	Cys			
				125					130						135		
Ser	Asp	Ser	Leu	Lys	Leu	Cys	Cys	Pro	Ala	Gly	Thr	Phe	Gly	Pro			
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Ser	Cys	Leu	Pro	Cys	Pro	Gly	Gly	Thr	Glu	Arg	Pro	Cys	Gly	Gly			
				155					160						165		
Tyr	Gly	Gln	Cys	Glu	Gly	Glu	Gly	Thr	Arg	Gly	Gly	Ser	Gly	His			
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Cys Asp Cys Gln Ala Gly Tyr Gly Gly Glu Ala Cys Gly Gln Cys
185 190 195

Gly Leu Gly Tyr Phe Glu Ala Glu Arg Asn Ala Ser His Leu Val
200 205 210

Cys Ser Ala Cys Phe Gly Pro Cys Ala Arg Cys Ser Gly Pro Glu
215 220 225

Glu Ser Asn Cys Leu Gln Cys Lys Lys Gly Trp Ala Leu His His
230 235 240

Leu Lys Cys Val Asp Ile Asp Glu Cys Gly Thr Glu Gly Ala Asn
245 250 255

Cys Gly Ala Asp Gln Phe Cys Val Asn Thr Glu Gly Ser Tyr Glu
260 265 270

Cys Arg Asp Cys Ala Lys Ala Cys Leu Gly Cys Met Gly Ala Gly
275 280 285

Pro Gly Arg Cys Lys Lys Cys Ser Pro Gly Tyr Gln Gln Val Gly
290 295 300

Ser Lys Cys Leu Asp Val Asp Glu Cys Glu Thr Glu Val Cys Pro
305 310 315

Gly Glu Asn Lys Gln Cys Glu Asn Thr Glu Gly Gly Tyr Arg Cys
320 325 330

Ile Cys Ala Glu Gly Tyr Lys Gln Met Glu Gly Ile Cys Val Lys
335 340 345

Glu Gln Ile Pro Glu Ser Ala Gly Phe Phe Ser Glu Met Thr Glu
350 355 360

Asp Glu Leu Val Val Leu Gln Gln Met Phe Phe Gly Ile Ile Ile
365 370 375

Cys Ala Leu Ala Thr Leu Ala Ala Lys Gly Asp Leu Val Phe Thr
380 385 390

Ala Ile Phe Ile Gly Ala Val Ala Ala Met Thr Gly Tyr Trp Leu
395 400 405

Ser Glu Arg Ser Asp Arg Val Leu Glu Gly Phe Ile Lys Gly Arg
410 415 420

<210> 110
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 110
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<210> 111
<211> 22
<212> DNA

<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 111
attctgcgtg aacactgagg gc 22

<210> 112
<211> 22
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<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 112
atctgcttgt agccctcggc ac 22

<210> 113
<211> 1616
<212> DNA
<213> Homo Sapien

<220>
<221> unsure
<222> 1461
<223> unknown base

<400> 113
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acatgagggt gcagaagtgc agctgtgcct cggatggtgc gctcgtgcca 1150

aggaggctcc agccataggc gcctagtgta gccatcgagg gacttgactt 1200

gtgtgtgttt ctgaagtgtt cgagggtacc aggagagctg gcgatgactg 1250

aactgctgat ggacaaatgc tctgtgctct ctagtgagcc ctgaatttgc 1300

ttcctctgac aagttacctc acctaatttt tgcttctcag gaatgagaat 1350

ctttggccac tggagagccc ttgctcagtt ttctctattc ttattattca 1400

ctgcactata ttctaagcac ttacatgtgg agatactgta acctgagggc 1450

agaaagccca ntgtgtcatt gtttacttgt cctgtcactg gatctgggct 1500

aaagtcctcc accaccactc tggacctaag acctggggtt aagtgtgggt 1550

tgtgcatccc caatccagat aataaagact ttgtaaaaca tgaataaaac 1600

acattttatt ctaaaa 1616

<210> 114
<211> 366
<212> PRT
<213> Homo Sapien

<400> 114

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Met Gln Pro Leu Trp Leu Cys Trp Ala Leu Trp Val Leu Pro Leu
  1               5                  10                  15

Ala Ser Pro Gly Ala Ala Leu Thr Gly Glu Gln Leu Leu Gly Ser
             20                  25                  30

Leu Leu Arg Gln Leu Gln Leu Lys Glu Val Pro Thr Leu Asp Arg
             35                  40                  45

Ala Asp Met Glu Glu Leu Val Ile Pro Thr His Val Arg Ala Gln
             50                  55                  60

Tyr Val Ala Leu Leu Gln Arg Ser His Gly Asp Arg Ser Arg Gly
             65                  70                  75

Lys Arg Phe Ser Gln Ser Phe Arg Glu Val Ala Gly Arg Phe Leu
             80                  85                  90

Ala Leu Glu Ala Ser Thr His Leu Leu Val Phe Gly Met Glu Gln
             95                 100                 105

Arg Leu Pro Pro Asn Ser Glu Leu Val Gln Ala Val Leu Arg Leu
            110                 115                 120
```

Phe Gln Glu Pro Val Pro Lys Ala Ala Leu His Arg His Gly Arg
125 130 135

Leu Ser Pro Arg Ser Ala Arg Ala Arg Val Thr Val Glu Trp Leu
140 145 150

Arg Val Arg Asp Asp Gly Ser Asn Arg Thr Ser Leu Ile Asp Ser
155 160 165

Arg Leu Val Ser Val His Glu Ser Gly Trp Lys Ala Phe Asp Val
170 175 180

Thr Glu Ala Val Asn Phe Trp Gln Gln Leu Ser Arg Pro Arg Gln
185 190 195

Pro Leu Leu Leu Gln Val Ser Val Gln Arg Glu His Leu Gly Pro
200 205 210

Leu Ala Ser Gly Ala His Lys Leu Val Arg Phe Ala Ser Gln Gly
215 220 225

Ala Pro Ala Gly Leu Gly Glu Pro Gln Leu Glu Leu His Thr Leu
230 235 240

Asp Leu Gly Asp Tyr Gly Ala Gln Gly Asp Cys Asp Pro Glu Ala
245 250 255

Pro Met Thr Glu Gly Thr Arg Cys Cys Arg Gln Glu Met Tyr Ile
260 265 270

Asp Leu Gln Gly Met Lys Trp Ala Glu Asn Trp Val Leu Glu Pro
275 280 285

Pro Gly Phe Leu Ala Tyr Glu Cys Val Gly Thr Cys Arg Gln Pro
290 295 300

Pro Glu Ala Leu Ala Phe Lys Trp Pro Phe Leu Gly Pro Arg Gln
305 310 315

Cys Ile Ala Ser Glu Thr Asp Ser Leu Pro Met Ile Val Ser Ile
320 325 330

Lys Glu Gly Gly Arg Thr Arg Pro Gln Val Val Ser Leu Pro Asn
335 340 345

Met Arg Val Gln Lys Cys Ser Cys Ala Ser Asp Gly Ala Leu Val
350 355 360

Pro Arg Arg Leu Gln Pro
365

<210> 115
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 115
aggactgcca taacttgcct g 21

<210> 116

<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 116
ataggagttg aagcagcgct gc 22

<210> 117
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 117
tgtgtggaca tagacgagtg ccgctaccgc tactgccagc accgc 45

<210> 118
<211> 1857
<212> DNA
<213> Homo Sapien

<400> 118
gtctgttccc aggagtcctt cggcggctgt tgtgtcagtg gcctgatcgc 50

gatggggaca aaggcgcaag tcgagaggaa actgttgtgc ctcttcatat 100

tggcgatcct gttgtgctcc ctggcattgg gcagtgttac agtgcactct 150

tctgaacctg aagtcagaat tcctgagaat aatcctgtga agttgtcctg 200

tgcctactcg ggcttttctt ctccccgtgt ggagtggaag tttgaccaag 250

gagacaccac cagactcgtt tgctataata acaagatcac agcttcctat 300

gaggaccggg tgaccttctt gccaactggt atcaccttca agtccgtgac 350

acgggaagac actgggacat acacttgtat ggtctctgag gaaggcggca 400

acagctatgg ggaggtcaag gtcaagctca tcgtgcttgt gcctccatcc 450

aagcctacag ttaacatccc ctcctctgcc accattggga accgggcagt 500

gctgacatgc tcagaacaag atggttcccc accttctgaa tacacctggt 550

tcaaagatgg gatagtgatg cctacgaatc ccaaaagcac ccgtgccttc 600

agcaactctt cctatgtcct gaatcccaca acaggagagc tggtctttga 650

tcccctgtca gcctctgata ctggagaata cagctgtgag gcacggaatg 700

ggtatgggac acccatgact tcaaatgctg tgcgcatgga agctgtggag 750

cggaatgtgg gggtcatcgt ggcagccgtc cttgtaaccc tgattctcct 800

gggaatcttg gtttttggca tctggtttgc ctatagccga ggccactttg 850

acagaacaaa gaaagggact tcgagtaaga aggtgattta cagccagcct 900

agtgcccgaa gtgaaggaga attcaaacag acctcgtcat tcctggtgtg 950

agcctggtcg gctcaccgcc tatcatctgc atttgcctta ctcaggtgct 1000

accggactct ggcccctgat gtctgtagtt tcacaggatg ccttatttgt 1050

cttctacacc ccacagggcc ccctacttct tcggatgtgt ttttaataat 1100

gtcagctatg tgccccatcc tccttcatgc cctccctccc tttcctacca 1150

ctgctgagtg gcctggaact tgtttaaagt gtttattccc catttctttg 1200

agggatcagg aaggaatcct gggtatgcca ttgacttccc ttctaagtag 1250

acagcaaaaa tggcgggggt cgcaggaatc tgcactcaac tgcccacctg 1300

gctggcaggg atctttgaat aggtatcttg agcttggttc tgggctcttt 1350

ccttgtgtac tgacgaccag ggccagctgt tctagagcgg gaattagagg 1400

ctagagcggc tgaaatggtt gtttggtgat gacactgggg tccttccatc 1450

tctggggccc actctcttct gtcttcccat gggaagtgcc actgggatcc 1500

ctctgccctg tcctcctgaa tacaagctga ctgacattga ctgtgtctgt 1550

ggaaaatggg agctcttgtt gtggagagca tagtaaattt tcagagaact 1600

tgaagccaaa aggatttaaa accgctgctc taaagaaaag aaaactggag 1650

gctgggcgca gtggctcacg cctgtaatcc cagaggctga ggcaggcgga 1700

tcacctgagg tcgggagttc gggatcagcc tgaccaacat ggagaaaccc 1750

tactggaaat acaaagttag ccaggcatgg tggtgcatgc ctgtagtccc 1800

agctgctcag gagcctggca acaagagcaa aactccagct caaaaaaaaa 1850

aaaaaaa 1857

<210> 119
<211> 299
<212> PRT
<213> Homo Sapien

<400> 119

Met	Gly	Thr	Lys	Ala	Gln	Val	Glu	Arg	Lys	Leu	Leu	Cys	Leu	Phe	
1				5				10						15	
Ile	Leu	Ala	Ile	Leu	Leu	Cys	Ser	Leu	Ala	Leu	Gly	Ser	Val	Thr	
			20					25						30	
Val	His	Ser	Ser	Glu	Pro	Glu	Val	Arg	Ile	Pro	Glu	Asn	Asn	Pro	
			35					40						45	
Val	Lys	Leu	Ser	Cys	Ala	Tyr	Ser	Gly	Phe	Ser	Ser	Pro	Arg	Val	
			50					55						60	
Glu	Trp	Lys	Phe	Asp	Gln	Gly	Asp	Thr	Thr	Arg	Leu	Val	Cys	Tyr	
			65					70						75	
Asn	Asn	Lys	Ile	Thr	Ala	Ser	Tyr	Glu	Asp	Arg	Val	Thr	Phe	Leu	
			80					85						90	

```
Pro Thr Gly Ile Thr Phe Lys Ser Val Thr Arg Glu Asp Thr Gly
                 95                  100                 105

Thr Tyr Thr Cys Met Val Ser Glu Glu Gly Gly Asn Ser Tyr Gly
            110                 115                 120

Glu Val Lys Val Lys Leu Ile Val Leu Val Pro Pro Ser Lys Pro
            125                 130                 135

Thr Val Asn Ile Pro Ser Ser Ala Thr Ile Gly Asn Arg Ala Val
            140                 145                 150

Leu Thr Cys Ser Glu Gln Asp Gly Ser Pro Pro Ser Glu Tyr Thr
            155                 160                 165

Trp Phe Lys Asp Gly Ile Val Met Pro Thr Asn Pro Lys Ser Thr
            170                 175                 180

Arg Ala Phe Ser Asn Ser Ser Tyr Val Leu Asn Pro Thr Thr Gly
            185                 190                 195

Glu Leu Val Phe Asp Pro Leu Ser Ala Ser Asp Thr Gly Glu Tyr
            200                 205                 210

Ser Cys Glu Ala Arg Asn Gly Tyr Gly Thr Pro Met Thr Ser Asn
            215                 220                 225

Ala Val Arg Met Glu Ala Val Glu Arg Asn Val Gly Val Ile Val
            230                 235                 240

Ala Ala Val Leu Val Thr Leu Ile Leu Leu Gly Ile Leu Val Phe
            245                 250                 255

Gly Ile Trp Phe Ala Tyr Ser Arg Gly His Phe Asp Arg Thr Lys
            260                 265                 270

Lys Gly Thr Ser Ser Lys Lys Val Ile Tyr Ser Gln Pro Ser Ala
            275                 280                 285

Arg Ser Glu Gly Glu Phe Lys Gln Thr Ser Ser Phe Leu Val
            290                 295

<210> 120
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 120
 tcgcggagct gtgttctgtt tccc 24

<210> 121
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 121
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tgatcgcgat ggggacaaag gcgcaagctc gagaggaaac tgttgtgcct 50

<210> 122
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 122
acacctggtt caaagatggg 20

<210> 123
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 123
taggaagagt tgctgaaggc acgg 24

<210> 124
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 124
ttgccttact caggtgctac 20

<210> 125
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 125
actcagcagt ggtaggaaag 20

<210> 126
<211> 1210
<212> DNA
<213> Homo Sapien

<400> 126
cagcgcgtgg ccggcgccgc tgtggggaca gcatgagcgg cggttggatg 50

gcgcaggttg gagcgtggcg aacaggggct ctgggcctgg cgctgctgct 100

gctgctcggc ctcggactag gcctggaggc cgccgcgagc ccgctttcca 150

ccccgacctc tgcccaggcc gcaggcccca gctcaggctc gtgcccaccc 200

accaagttcc agtgccgcac cagtggctta tgcgtgcccc tcacctggcg 250

ctgcgacagg gacttggact gcagcgatgg cagcgatgag gaggagtgca 300

ggattgagcc atgtacccag aaagggcaat gcccaccgcc ccctggcctc 350

ccctgccccc gcaccggcgt cagtgactgc tctgggggaa ctgacaagaa 400

actgcgcaac tgcagccgcc tggcctgcct agcaggcgag ctccgttgca 450

cgctgagcga tgactgcatt ccactcacgt ggcgctgcga cggccaccca 500

gactgtcccg actccagcga cgagctcggc tgtggaacca atgagatcct 550

cccggaaggg gatgccacaa ccatggggcc ccctgtgacc ctggagagtg 600

tcacctctct caggaatgcc acaaccatgg ggccccctgt gaccctggag 650

agtgtccccc ctgtcgggaa tgccacatcc tcctctgccg gagaccagtc 700

tggaagccca actgcctatg gggttattgc agctgctgcg gtgctcagtg 750

caagcctggt caccgccacc ctcctccttt tgtcctggct ccgagcccag 800

gagcgcctcc gcccactggg gttactggtg gccatgaagg agtccctgct 850

gctgtcagaa cagaagacct cgctgccctg aggacaagca cttgccacca 900

ccgtcactca gccctgggcg tagccggaca ggaggagagc agtgatgcgg 950

atgggtaccc gggcacacca gccctcagag acctgagttc ttctggccac 1000

gtggaacctc gaacccgagc tcctgcagaa gtggccctgg agattgaggg 1050

tccctggaca ctccctatgg agatccgggg agctaggatg gggaacctgc 1100

cacagccaga actgaggggc tggccccagg cagctcccag ggggtagaac 1150

ggccctgtgc ttaagacact ccctgctgcc ccgtctgagg gtggcgatta 1200

aagttgcttc 1210

<210> 127
<211> 282
<212> PRT
<213> Homo Sapien

<400> 127

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Met Ser Gly Gly Trp Met Ala Gln Val Gly Ala Trp Arg Thr Gly
  1               5                  10                  15

Ala Leu Gly Leu Ala Leu Leu Leu Leu Leu Gly Leu Gly Leu Gly
             20                  25                  30

Leu Glu Ala Ala Ala Ser Pro Leu Ser Thr Pro Thr Ser Ala Gln
             35                  40                  45

Ala Ala Gly Pro Ser Ser Gly Ser Cys Pro Pro Thr Lys Phe Gln
             50                  55                  60

Cys Arg Thr Ser Gly Leu Cys Val Pro Leu Thr Trp Arg Cys Asp
             65                  70                  75

Arg Asp Leu Asp Cys Ser Asp Gly Ser Asp Glu Glu Glu Cys Arg
             80                  85                  90
```

Ile Glu Pro Cys Thr Gln Lys Gly Gln Cys Pro Pro Pro Pro Gly
95 100 105

Leu Pro Cys Pro Cys Thr Gly Val Ser Asp Cys Ser Gly Gly Thr
110 115 120

Asp Lys Lys Leu Arg Asn Cys Ser Arg Leu Ala Cys Leu Ala Gly
125 130 135

Glu Leu Arg Cys Thr Leu Ser Asp Asp Cys Ile Pro Leu Thr Trp
140 145 150

Arg Cys Asp Gly His Pro Asp Cys Pro Asp Ser Ser Asp Glu Leu
155 160 165

Gly Cys Gly Thr Asn Glu Ile Leu Pro Glu Gly Asp Ala Thr Thr
170 175 180

Met Gly Pro Pro Val Thr Leu Glu Ser Val Thr Ser Leu Arg Asn
185 190 195

Ala Thr Thr Met Gly Pro Pro Val Thr Leu Glu Ser Val Pro Ser
200 205 210

Val Gly Asn Ala Thr Ser Ser Ser Ala Gly Asp Gln Ser Gly Ser
215 220 225

Pro Thr Ala Tyr Gly Val Ile Ala Ala Ala Ala Val Leu Ser Ala
230 235 240

Ser Leu Val Thr Ala Thr Leu Leu Leu Leu Ser Trp Leu Arg Ala
245 250 255

Gln Glu Arg Leu Arg Pro Leu Gly Leu Leu Val Ala Met Lys Glu
260 265 270

Ser Leu Leu Leu Ser Glu Gln Lys Thr Ser Leu Pro
275 280

<210> 128
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 128
aagttccagt gccgcaccag tggc 24

<210> 129
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 129
ttggttccac agccgagctc gtcg 24

<210> 130
<211> 50

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 130
gaggaggagt gcaggattga gccatgtacc cagaaagggc aatgcccacc 50

<210> 131
<211> 1843
<212> DNA
<213> Homo Sapien

<220>
<221> unsure
<222> 1837
<223> unknown base

<400> 131
cccacgcgtc cggtctcgct cgctcgcgca gcggcggcag cagaggtcgc 50

gcacagatgc gggttagact ggcgggggga ggaggcggag gagggaagga 100

agctgcatgc atgagaccca cagactcttg caagctggat gccctctgtg 150

gatgaaagat gtatcatgga atgaacccga gcaatggaga tggatttcta 200

gagcagcagc agcagcagca gcaacctcag tccccccaga gactcttggc 250

cgtgatcctg tggtttcagc tggcgctgtg cttcggccct gcacagctca 300

cgggcgggtt cgatgacctt caagtgtgtg ctgaccccgg cattcccgag 350

aatggcttca ggacccccag cggaggggtt ttctttgaag gctctgtagc 400

ccgatttcac tgccaagacg gattcaagct gaagggcgct acaaagagac 450

tgtgtttgaa gcattttaat ggaaccctag gctggatccc aagtgataat 500

tccatctgtg tgcaagaaga ttgccgtatc cctcaaatcg aagatgctga 550

gattcataac aagacatata gacatggaga gaagctaatc atcacttgtc 600

atgaaggatt caagatccgg taccccgacc tacacaatat ggtttcatta 650

tgtcgcgatg atggaacgtg gaataatctg cccatctgtc aaggctgcct 700

gagacctcta gcctcttcta atggctatgt aaacatctct gagctccaga 750

cctccttccc ggtggggact gtgatctcct atcgctgctt tcccggattt 800

aaacttgatg ggtctgcgta tcttgagtgc ttacaaaacc ttatctggtc 850

gtccagccca ccccggtgcc ttgctctgga agcccaagtc tgtccactac 900

ctccaatggt gagtcacgga gatttcgtct gccacccgcg gccttgtgag 950

cgctacaacc acggaactgt ggtggagttt tactgcgatc ctggctacag 1000

cctcaccagc gactacaagt acatcacctg ccagtatgga gagtggtttc 1050

cttcttatca agtctactgc atcaaatcag agcaaacgtg gcccagcacc 1100

catgagaccc tcctgaccac gtggaagatt gtggcgttca cggcaaccag 1150

tgtgctgctg gtgctgctgc tcgtcatcct ggccaggatg ttccagacca 1200

agttcaaggc ccactttccc cccagggggc ctccccggag ttccagcagt 1250

gaccctgact ttgtggtggt agacggcgtg cccgtcatgc tcccgtccta 1300

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cctctgtggg ccagggctgc cccttacccg tggacgacca gagcccccca 1400

gcataccccg gctcagggga cacggacaca ggcccagggg agtcagaaac 1450

ctgtgacagc gtctcaggct cttctgagct gctccaaagt ctgtattcac 1500

ctcccaggtg ccaagagagc acccaccctg cttcggacaa ccctgacata 1550

attgccagca cggcagagga ggtggcatcc accagcccag gcatccatca 1600

tgcccactgg gtgttgttcc taagaaactg attgattaaa aaatttccca 1650

aagtgtcctg aagtgtctct tcaaatacat gttgatctgt ggagttgatt 1700

cctttccttc tcttggtttt agacaaatgt aaacaaagct ctgatcctta 1750

aaattgctat gctgatagag tggtgagggc tggaagcttg atcaagtcct 1800

gtttcttctt gacacagact gattaaaaat taaaagnaaa aaa 1843

<210> 132
<211> 490
<212> PRT
<213> Homo Sapien

<400> 132

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Met Tyr His Gly Met Asn Pro Ser Asn Gly Asp Gly Phe Leu Glu
  1               5                  10                  15

Gln Gln Gln Gln Gln Gln Gln Pro Gln Ser Pro Gln Arg Leu Leu
                20                  25                  30

Ala Val Ile Leu Trp Phe Gln Leu Ala Leu Cys Phe Gly Pro Ala
                35                  40                  45

Gln Leu Thr Gly Gly Phe Asp Asp Leu Gln Val Cys Ala Asp Pro
                50                  55                  60

Gly Ile Pro Glu Asn Gly Phe Arg Thr Pro Ser Gly Gly Val Phe
                65                  70                  75

Phe Glu Gly Ser Val Ala Arg Phe His Cys Gln Asp Gly Phe Lys
                80                  85                  90

Leu Lys Gly Ala Thr Lys Arg Leu Cys Leu Lys His Phe Asn Gly
                95                 100                 105

Thr Leu Gly Trp Ile Pro Ser Asp Asn Ser Ile Cys Val Gln Glu
               110                 115                 120

Asp Cys Arg Ile Pro Gln Ile Glu Asp Ala Glu Ile His Asn Lys
               125                 130                 135
```

```
Thr Tyr Arg His Gly Glu Lys Leu Ile Ile Thr Cys His Glu Gly
                140                 145                 150

Phe Lys Ile Arg Tyr Pro Asp Leu His Asn Met Val Ser Leu Cys
                155                 160                 165

Arg Asp Asp Gly Thr Trp Asn Asn Leu Pro Ile Cys Gln Gly Cys
                170                 175                 180

Leu Arg Pro Leu Ala Ser Ser Asn Gly Tyr Val Asn Ile Ser Glu
                185                 190                 195

Leu Gln Thr Ser Phe Pro Val Gly Thr Val Ile Ser Tyr Arg Cys
                200                 205                 210

Phe Pro Gly Phe Lys Leu Asp Gly Ser Ala Tyr Leu Glu Cys Leu
                215                 220                 225

Gln Asn Leu Ile Trp Ser Ser Ser Pro Pro Arg Cys Leu Ala Leu
                230                 235                 240

Glu Ala Gln Val Cys Pro Leu Pro Pro Met Val Ser His Gly Asp
                245                 250                 255

Phe Val Cys His Pro Arg Pro Cys Glu Arg Tyr Asn His Gly Thr
                260                 265                 270

Val Val Glu Phe Tyr Cys Asp Pro Gly Tyr Ser Leu Thr Ser Asp
                275                 280                 285

Tyr Lys Tyr Ile Thr Cys Gln Tyr Gly Glu Trp Phe Pro Ser Tyr
                290                 295                 300

Gln Val Tyr Cys Ile Lys Ser Glu Gln Thr Trp Pro Ser Thr His
                305                 310                 315

Glu Thr Leu Leu Thr Thr Trp Lys Ile Val Ala Phe Thr Ala Thr
                320                 325                 330

Ser Val Leu Leu Val Leu Leu Leu Val Ile Leu Ala Arg Met Phe
                335                 340                 345

Gln Thr Lys Phe Lys Ala His Phe Pro Pro Arg Gly Pro Pro Arg
                350                 355                 360

Ser Ser Ser Ser Asp Pro Asp Phe Val Val Val Asp Gly Val Pro
                365                 370                 375

Val Met Leu Pro Ser Tyr Asp Glu Ala Val Ser Gly Gly Leu Ser
                380                 385                 390

Ala Leu Gly Pro Gly Tyr Met Ala Ser Val Gly Gln Gly Cys Pro
                395                 400                 405

Leu Pro Val Asp Asp Gln Ser Pro Pro Ala Tyr Pro Gly Ser Gly
                410                 415                 420

Asp Thr Asp Thr Gly Pro Gly Glu Ser Glu Thr Cys Asp Ser Val
                425                 430                 435

Ser Gly Ser Ser Glu Leu Leu Gln Ser Leu Tyr Ser Pro Pro Arg
                440                 445                 450
```

Cys Gln Glu Ser Thr His Pro Ala Ser Asp Asn Pro Asp Ile Ile
455 460 465

Ala Ser Thr Ala Glu Glu Val Ala Ser Thr Ser Pro Gly Ile His
470 475 480

His Ala His Trp Val Leu Phe Leu Arg Asn
485 490

<210> 133
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 133
atctcctatc gctgctttcc cgg 23

<210> 134
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 134
agccaggatc gcagtaaaac tcc 23

<210> 135
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 135
atttaaactt gatgggtctg cgtatcttga gtgcttacaa aaccttatct 50

<210> 136
<211> 1815
<212> DNA
<213> Homo Sapien

<400> 136
cccacgcgtc cgctccgcgc cctccccccc gcctcccgtg cggtccgtcg 50

gtggcctaga gatgctgctg ccgcggttgc agttgtcgcg cacgcctctg 100

cccgccagcc cgctccaccg ccgtagcgcc cgagtgtcgg ggggcgcacc 150

cgagtcgggc catgaggccg ggaaccgcgc tacaggccgt gctgctggcc 200

gtgctgctgg tggggctgcg ggccgcgacg ggtcgcctgc tgagtgcctc 250

ggatttggac ctcagaggag ggcagccagt ctgccgggga gggacacaga 300

ggccttgtta taaagtcatt tacttccatg atacttctcg aagactgaac 350

tttgaggaag ccaaagaagc ctgcaggagg gatggaggcc agctagtcag 400

catcgagtct gaagatgaac agaaactgat agaaaagttc attgaaaacc 450

tcttgccatc tgatggtgac ttctggattg ggctcaggag gcgtgaggag 500

aaacaaagca atagcacagc ctgccaggac ctttatgctt ggactgatgg 550

cagcatatca caatttagga actggtatgt ggatgagccg tcctgcggca 600

gcgaggtctg cgtggtcatg taccatcagc catcggcacc cgctggcatc 650

ggaggcccct acatgttcca gtggaatgat gaccggtgca acatgaagaa 700

caatttcatt tgcaaatatt ctgatgagaa accagcagtt ccttctagag 750

aagctgaagg tgaggaaaca gagctgacaa cacctgtact tccagaagaa 800

acacaggaag aagatgccaa aaaaacattt aaagaaagta gagaagctgc 850

cttgaatctg gcctacatcc taatccccag cattcccctt ctcctcctcc 900

ttgtggtcac cacagttgta tgttgggttt ggatctgtag aaaaagaaaa 950

cgggagcagc cagaccctag cacaaagaag caacacacca tctggccctc 1000

tcctcaccag ggaaacagcc cggacctaga ggtctacaat gtcataagaa 1050

aacaaagcga agctgactta gctgagaccc ggccagacct gaagaatatt 1100

tcattccgag tgtgttcggg agaagccact cccgatgaca tgtcttgtga 1150

ctatgacaac atggctgtga acccatcaga aagtgggttt gtgactctgg 1200

tgagcgtgga gagtggattt gtgaccaatg acatttatga gttctcccca 1250

gaccaaatgg ggaggagtaa ggagtctgga tgggtggaaa atgaaatata 1300

tggttattag gacatataaa aaactgaaac tgacaacaat ggaaaagaaa 1350

tgataagcaa aatcctctta ttttctataa ggaaaataca cagaaggtct 1400

atgaacaagc ttagatcagg tcctgtggat gagcatgtgg tccccacgac 1450

ctcctgttgg acccccacgt tttggctgta tcctttatcc cagccagtca 1500

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ctctgttttc cttgctctat acagcagcac atattatcat acagacagaa 1700

aatccagaat cttttcaaag cccacatatg gtagcacagg ttggcctgtg 1750

catcggcaat tctcatatct gtttttttca aagaataaaa tcaaataaag 1800

agcaggaaaa aaaaa 1815

<210> 137
<211> 382
<212> PRT

<213> Homo Sapien

<400> 137

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 Met Arg Pro Gly Thr Ala Leu Gln Ala Val Leu Leu Ala Val Leu
   1               5                  10                  15

 Leu Val Gly Leu Arg Ala Ala Thr Gly Arg Leu Leu Ser Ala Ser
                20                  25                  30

 Asp Leu Asp Leu Arg Gly Gly Gln Pro Val Cys Arg Gly Gly Thr
                35                  40                  45

 Gln Arg Pro Cys Tyr Lys Val Ile Tyr Phe His Asp Thr Ser Arg
                50                  55                  60

 Arg Leu Asn Phe Glu Glu Ala Lys Glu Ala Cys Arg Arg Asp Gly
                65                  70                  75

 Gly Gln Leu Val Ser Ile Glu Ser Glu Asp Glu Gln Lys Leu Ile
                80                  85                  90

 Glu Lys Phe Ile Glu Asn Leu Leu Pro Ser Asp Gly Asp Phe Trp
                95                 100                 105

 Ile Gly Leu Arg Arg Arg Glu Glu Lys Gln Ser Asn Ser Thr Ala
               110                 115                 120

 Cys Gln Asp Leu Tyr Ala Trp Thr Asp Gly Ser Ile Ser Gln Phe
               125                 130                 135

 Arg Asn Trp Tyr Val Asp Glu Pro Ser Cys Gly Ser Glu Val Cys
               140                 145                 150

 Val Val Met Tyr His Gln Pro Ser Ala Pro Ala Gly Ile Gly Gly
               155                 160                 165

 Pro Tyr Met Phe Gln Trp Asn Asp Asp Arg Cys Asn Met Lys Asn
               170                 175                 180

 Asn Phe Ile Cys Lys Tyr Ser Asp Glu Lys Pro Ala Val Pro Ser
               185                 190                 195

 Arg Glu Ala Glu Gly Glu Glu Thr Glu Leu Thr Thr Pro Val Leu
               200                 205                 210

 Pro Glu Glu Thr Gln Glu Glu Asp Ala Lys Lys Thr Phe Lys Glu
               215                 220                 225

 Ser Arg Glu Ala Ala Leu Asn Leu Ala Tyr Ile Leu Ile Pro Ser
               230                 235                 240

 Ile Pro Leu Leu Leu Leu Leu Val Val Thr Thr Val Val Cys Trp
               245                 250                 255

 Val Trp Ile Cys Arg Lys Arg Lys Arg Glu Gln Pro Asp Pro Ser
               260                 265                 270

 Thr Lys Lys Gln His Thr Ile Trp Pro Ser Pro His Gln Gly Asn
               275                 280                 285

 Ser Pro Asp Leu Glu Val Tyr Asn Val Ile Arg Lys Gln Ser Glu
               290                 295                 300
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Ala Asp Leu Ala Glu Thr Arg Pro Asp Leu Lys Asn Ile Ser Phe
305 310 315

Arg Val Cys Ser Gly Glu Ala Thr Pro Asp Asp Met Ser Cys Asp
320 325 330

Tyr Asp Asn Met Ala Val Asn Pro Ser Glu Ser Gly Phe Val Thr
335 340 345

Leu Val Ser Val Glu Ser Gly Phe Val Thr Asn Asp Ile Tyr Glu
350 355 360

Phe Ser Pro Asp Gln Met Gly Arg Ser Lys Glu Ser Gly Trp Val
365 370 375

Glu Asn Glu Ile Tyr Gly Tyr
380

<210> 138
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 138
gttcattgaa aacctcttgc catctgatgg tgacttctgg attgggctca 50

<210> 139
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 139
aagccaaaga agcctgcagg aggg 24

<210> 140
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 140
cagtccaagc ataaaggtcc tggc 24

<210> 141
<211> 1514
<212> DNA
<213> Homo Sapien

<400> 141
ggggtctccc tcagggccgg gaggcacagc ggtccctgct tgctgaaggg 50

ctggatgtac gcatccgcag gttcccgcgg acttgggggc gcccgctgag 100

ccccggcgcc cgcagaagac ttgtgtttgc ctcctgcagc ctcaacccgg 150

agggcagcga gggcctacca ccatgatcac tggtgtgttc agcatgcgct 200

tgtggacccc agtgggcgtc ctgacctcgc tggcgtactg cctgcaccag 250

cggcgggtgg ccctggccga gctgcaggag gccgatggcc agtgtccggt 300

cgaccgcagc ctgctgaagt tgaaaatggt gcaggtcgtg tttcgacacg 350

gggctcggag tcctctcaag ccgctcccgc tggaggagca ggtagagtgg 400

aacccccagc tattagaggt cccaccccaa actcagtttg attacacagt 450

caccaatcta gctggtggtc cgaaaccata ttctccttac gactctcaat 500

accatgagac caccctgaag gggggcatgt ttgctgggca gctgaccaag 550

gtgggcatgc agcaaatgtt tgccttggga gagagactga ggaagaacta 600

tgtggaagac attccctttc tttcaccaac cttcaaccca caggaggtct 650

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ctggctgggc ttttccagtg tcagaaagaa ggacccatca tcatccacac 750

tgatgaagca gattcagaag tcttgtatcc caactaccaa agctgctgga 800

gcctgaggca gagaaccaga ggccggaggc agactgcctc tttacagcca 850

ggaatctcag aggatttgaa aaaggtgaag gacaggatgg gcattgacag 900

tagtgataaa gtggacttct tcatcctcct ggacaacgtg gctgccgagc 950

aggcacacaa cctcccaagc tgccccatgc tgaagagatt tgcacggatg 1000

atcgaacaga gagctgtgga cacatccttg tacatactgc ccaaggaaga 1050

cagggaaagt cttcagatgg cagtaggccc attcctccac atcctagaga 1100

gcaacctgct gaaagccatg gactctgcca ctgcccccga caagatcaga 1150

aagctgtatc tctatgcggc tcatgatgtg accttcatac cgctcttaat 1200

gaccctgggg atttttgacc acaaatggcc accgtttgct gttgacctga 1250

ccatggaact ttaccagcac ctggaatcta aggagtggtt tgtgcagctc 1300

tattaccacg ggaaggagca ggtgccgaga ggttgccctg atgggctctg 1350

cccgctggac atgttcttga atgccatgtc agtttatacc ttaagcccag 1400

aaaaatacca tgcactctgc tctcaaactc aggtgatgga agttggaaat 1450

gaagagtaac tgatttataa aagcaggatg tgttgatttt aaaataaagt 1500

gcctttatac aatg 1514

<210> 142
<211> 428
<212> PRT
<213> Homo Sapien

<400> 142
Met Ile Thr Gly Val Phe Ser Met Arg Leu Trp Thr Pro Val Gly

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  1               5                  10                  15

Val Leu Thr Ser Leu Ala Tyr Cys Leu His Gln Arg Arg Val Ala
                20                  25                  30

Leu Ala Glu Leu Gln Glu Ala Asp Gly Gln Cys Pro Val Asp Arg
                35                  40                  45

Ser Leu Leu Lys Leu Lys Met Val Gln Val Val Phe Arg His Gly
                50                  55                  60

Ala Arg Ser Pro Leu Lys Pro Leu Pro Leu Glu Glu Gln Val Glu
                65                  70                  75

Trp Asn Pro Gln Leu Leu Glu Val Pro Pro Gln Thr Gln Phe Asp
                80                  85                  90

Tyr Thr Val Thr Asn Leu Ala Gly Gly Pro Lys Pro Tyr Ser Pro
                95                 100                 105

Tyr Asp Ser Gln Tyr His Glu Thr Thr Leu Lys Gly Gly Met Phe
               110                 115                 120

Ala Gly Gln Leu Thr Lys Val Gly Met Gln Gln Met Phe Ala Leu
               125                 130                 135

Gly Glu Arg Leu Arg Lys Asn Tyr Val Glu Asp Ile Pro Phe Leu
               140                 145                 150

Ser Pro Thr Phe Asn Pro Gln Glu Val Phe Ile Arg Ser Thr Asn
               155                 160                 165

Ile Phe Arg Asn Leu Glu Ser Thr Arg Cys Leu Leu Ala Gly Leu
               170                 175                 180

Phe Gln Cys Gln Lys Glu Gly Pro Ile Ile Ile His Thr Asp Glu
               185                 190                 195

Ala Asp Ser Glu Val Leu Tyr Pro Asn Tyr Gln Ser Cys Trp Ser
               200                 205                 210

Leu Arg Gln Arg Thr Arg Gly Arg Arg Gln Thr Ala Ser Leu Gln
               215                 220                 225

Pro Gly Ile Ser Glu Asp Leu Lys Lys Val Lys Asp Arg Met Gly
               230                 235                 240

Ile Asp Ser Ser Asp Lys Val Asp Phe Phe Ile Leu Leu Asp Asn
               245                 250                 255

Val Ala Ala Glu Gln Ala His Asn Leu Pro Ser Cys Pro Met Leu
               260                 265                 270

Lys Arg Phe Ala Arg Met Ile Glu Gln Arg Ala Val Asp Thr Ser
               275                 280                 285

Leu Tyr Ile Leu Pro Lys Glu Asp Arg Glu Ser Leu Gln Met Ala
               290                 295                 300

Val Gly Pro Phe Leu His Ile Leu Glu Ser Asn Leu Leu Lys Ala
               305                 310                 315

Met Asp Ser Ala Thr Ala Pro Asp Lys Ile Arg Lys Leu Tyr Leu
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320 325 330

Tyr Ala Ala His Asp Val Thr Phe Ile Pro Leu Leu Met Thr Leu
335 340 345

Gly Ile Phe Asp His Lys Trp Pro Pro Phe Ala Val Asp Leu Thr
350 355 360

Met Glu Leu Tyr Gln His Leu Glu Ser Lys Glu Trp Phe Val Gln
365 370 375

Leu Tyr Tyr His Gly Lys Glu Gln Val Pro Arg Gly Cys Pro Asp
380 385 390

Gly Leu Cys Pro Leu Asp Met Phe Leu Asn Ala Met Ser Val Tyr
395 400 405

Thr Leu Ser Pro Glu Lys Tyr His Ala Leu Cys Ser Gln Thr Gln
410 415 420

Val Met Glu Val Gly Asn Glu Glu
425

<210> 143
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 143
ccaactacca aagctgctgg agcc 24

<210> 144
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 144
gcagctctat taccacggga agga 24

<210> 145
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 145
tccttcccgt ggtaatagag ctgc 24

<210> 146
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 146
ggcagagaac cagaggccgg aggagactgc ctctttacag ccagg 45

<210> 147
<211> 1686
<212> DNA
<213> Homo Sapien

<400> 147
ctcctcttaa catacttgca gctaaaacta aatattgctg cttggggacc 50

tccttctagc cttaaatttc agctcatcac cttcacctgc cttggtcatg 100

gctctgctat tctccttgat ccttgccatt tgcaccagac ctggattcct 150

agcgtctcca tctggagtgc ggctggtggg gggcctccac cgctgtgaag 200

ggcgggtgga ggtggaacag aaaggccagt ggggcaccgt gtgtgatgac 250

ggctgggaca ttaaggacgt ggctgtgttg tgccgggagc tgggctgtgg 300

agctgccagc ggaaccccta gtggtatttt gtatgagcca ccagcagaaa 350

aagagcaaaa ggtcctcatc caatcagtca gttgcacagg aacagaagat 400

acattggctc agtgtgagca agaagaagtt tatgattgtt cacatgatga 450

agatgctggg gcatcgtgtg agaacccaga gagctctttc tccccagtcc 500

cagagggtgt caggctggct gacggccctg ggcattgcaa gggacgcgtg 550

gaagtgaagc accagaacca gtggtatacc gtgtgccaga caggctggag 600

cctccgggcc gcaaaggtgg tgtgccggca gctgggatgt gggagggctg 650

tactgactca aaaacgctgc aacaagcatg cctatggccg aaaacccatc 700

tggctgagcc agatgtcatg ctcaggacga gaagcaaccc ttcaggattg 750

cccttctggg ccttggggga agaacacctg caaccatgat gaagacacgt 800

gggtcgaatg tgaagatccc tttgacttga gactagtagg aggagacaac 850

ctctgctctg ggcgactgga ggtgctgcac aagggcgtat ggggctctgt 900

ctgtgatgac aactggggag aaaaggagga ccaggtggta tgcaagcaac 950

tgggctgtgg gaagtccctc tctccctcct tcagagaccg gaaatgctat 1000

ggccctgggg ttggccgcat ctggctggat aatgttcgtt gctcagggga 1050

ggagcagtcc ctggagcagt gccagcacag attttggggg tttcacgact 1100

gcacccacca ggaagatgtg gctgtcatct gctcagtgta ggtgggcatc 1150

atctaatctg ttgagtgcct gaatagaaga aaaacacaga agaagggagc 1200

atttactgtc tacatgactg catgggatga acactgatct tcttctgccc 1250

ttggactggg acttatactt ggtgcccctg attctcaggc cttcagagtt 1300

ggatcagaac ttacaacatc aggtctagtt ctcaggccat cagacatagt 1350

ttggaactac atcaccacct ttcctatgtc tccacattgc acacagcaga 1400

ttcccagcct ccataattgt gtgtatcaac tacttaaata cattctcaca 1450

cacacacaca cacacacaca cacacacaca cacacataca ccatttgtcc 1500

tgtttctctg aagaactctg acaaaataca gattttggta ctgaaagaga 1550

ttctagagga acggaatttt aaggataaat tttctgaatt ggttatgggg 1600

tttctgaaat tggctctata atctaattag atataaaatt ctggtaactt 1650

tatttacaat aataaagata gcactatgtg ttcaaa 1686

<210> 148
<211> 347
<212> PRT
<213> Homo Sapien

<400> 148

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Met Ala Leu Leu Phe Ser Leu Ile Leu Ala Ile Cys Thr Arg Pro
  1               5                  10                  15

Gly Phe Leu Ala Ser Pro Ser Gly Val Arg Leu Val Gly Gly Leu
             20                  25                  30

His Arg Cys Glu Gly Arg Val Glu Val Glu Gln Lys Gly Gln Trp
             35                  40                  45

Gly Thr Val Cys Asp Asp Gly Trp Asp Ile Lys Asp Val Ala Val
             50                  55                  60

Leu Cys Arg Glu Leu Gly Cys Gly Ala Ala Ser Gly Thr Pro Ser
             65                  70                  75

Gly Ile Leu Tyr Glu Pro Pro Ala Glu Lys Glu Gln Lys Val Leu
             80                  85                  90

Ile Gln Ser Val Ser Cys Thr Gly Thr Glu Asp Thr Leu Ala Gln
             95                 100                 105

Cys Glu Gln Glu Glu Val Tyr Asp Cys Ser His Asp Glu Asp Ala
            110                 115                 120

Gly Ala Ser Cys Glu Asn Pro Glu Ser Ser Phe Ser Pro Val Pro
            125                 130                 135

Glu Gly Val Arg Leu Ala Asp Gly Pro Gly His Cys Lys Gly Arg
            140                 145                 150

Val Glu Val Lys His Gln Asn Gln Trp Tyr Thr Val Cys Gln Thr
            155                 160                 165

Gly Trp Ser Leu Arg Ala Ala Lys Val Val Cys Arg Gln Leu Gly
            170                 175                 180

Cys Gly Arg Ala Val Leu Thr Gln Lys Arg Cys Asn Lys His Ala
            185                 190                 195

Tyr Gly Arg Lys Pro Ile Trp Leu Ser Gln Met Ser Cys Ser Gly
            200                 205                 210
```

Arg Glu Ala Thr Leu Gln Asp Cys Pro Ser Gly Pro Trp Gly Lys
215 220 225

Asn Thr Cys Asn His Asp Glu Asp Thr Trp Val Glu Cys Glu Asp
230 235 240

Pro Phe Asp Leu Arg Leu Val Gly Gly Asp Asn Leu Cys Ser Gly
245 250 255

Arg Leu Glu Val Leu His Lys Gly Val Trp Gly Ser Val Cys Asp
260 265 270

Asp Asn Trp Gly Glu Lys Glu Asp Gln Val Val Cys Lys Gln Leu
275 280 285

Gly Cys Gly Lys Ser Leu Ser Pro Ser Phe Arg Asp Arg Lys Cys
290 295 300

Tyr Gly Pro Gly Val Gly Arg Ile Trp Leu Asp Asn Val Arg Cys
305 310 315

Ser Gly Glu Glu Gln Ser Leu Glu Gln Cys Gln His Arg Phe Trp
320 325 330

Gly Phe His Asp Cys Thr His Gln Glu Asp Val Ala Val Ile Cys
335 340 345

Ser Val

<210> 149
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 149
ttcagctcat caccttcacc tgcc 24

<210> 150
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 150
ggctcataca aaataccact aggg 24

<210> 151
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 151
gggcctccac cgctgtgaag ggcgggtgga ggtggaacag aaaggccagt 50

<210> 152
<211> 1427
<212> DNA
<213> Homo Sapien

<400> 152
actgcactcg gttctatcga ttgaattccc cggggatcct ctagagatcc 50

ctcgacctcg acccacgcgt ccgcggacgc gtgggcggac gcgtgggccg 100

gctaccagga agagtctgcc gaaggtgaag gccatggact tcatcacctc 150

cacagccatc ctgcccctgc tgttcggctg cctgggcgtc ttcggcctct 200

tccggctgct gcagtgggtg cgcgggaagg cctacctgcg gaatgctgtg 250

gtggtgatca caggcgccac ctcagggctg ggcaaagaat gtgcaaaagt 300

cttctatgct gcgggtgcta aactggtgct ctgtggccgg aatggtgggg 350

ccctagaaga gctcatcaga gaacttaccg cttctcatgc caccaaggtg 400

cagacacaca agccttactt ggtgaccttc gacctcacag actctggggc 450

catagttgca gcagcagctg agatcctgca gtgctttggc tatgtcgaca 500

tacttgtcaa caatgctggg atcagctacc gtggtaccat catggacacc 550

acagtggatg tggacaagag ggtcatggag acaaactact ttggcccagt 600

tgctctaacg aaagcactcc tgccctccat gatcaagagg aggcaaggcc 650

acattgtcgc catcagcagc atccagggca agatgagcat tccttttcga 700

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gctacatcca caccaacctc tctgtaaatg ccatcaccgc ggatggatct 850

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tcctggctga cttactgcct tccttggctg tttatcttcg aactctggct 1000

cctgggctct tcttcagcct catggcctcc agggccagaa aagagcggaa 1050

atccaagaac tcctagtact ctgaccagcc agggccaggg cagagaagca 1100

gcactcttag gcttgcttac tctacaaggg acagttgcat ttgttgagac 1150

tttaatggag atttgtctca caagtgggaa agactgaaga aacacatctc 1200

gtgcagatct gctggcagag gacaatcaaa aacgacaaca agcttcttcc 1250

cagggtgagg ggaaacactt aaggaataaa tatggagctg gggtttaaca 1300

ctaaaaacta gaaataaaca tctcaaacag taaaaaaaaa aaaaaagggc 1350

ggccgcgact ctagagtcga cctgcagaag cttggccgcc atggcccaac 1400

ttgtttattg cagcttataa tggttac 1427

<210> 153
<211> 310
<212> PRT
<213> Homo Sapien

<400> 153

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Met Asp Phe Ile Thr Ser Thr Ala Ile Leu Pro Leu Leu Phe Gly
  1               5                  10                  15

Cys Leu Gly Val Phe Gly Leu Phe Arg Leu Leu Gln Trp Val Arg
             20                  25                  30

Gly Lys Ala Tyr Leu Arg Asn Ala Val Val Val Ile Thr Gly Ala
             35                  40                  45

Thr Ser Gly Leu Gly Lys Glu Cys Ala Lys Val Phe Tyr Ala Ala
             50                  55                  60

Gly Ala Lys Leu Val Leu Cys Gly Arg Asn Gly Gly Ala Leu Glu
             65                  70                  75

Glu Leu Ile Arg Glu Leu Thr Ala Ser His Ala Thr Lys Val Gln
             80                  85                  90

Thr His Lys Pro Tyr Leu Val Thr Phe Asp Leu Thr Asp Ser Gly
             95                 100                 105

Ala Ile Val Ala Ala Ala Ala Glu Ile Leu Gln Cys Phe Gly Tyr
            110                 115                 120

Val Asp Ile Leu Val Asn Asn Ala Gly Ile Ser Tyr Arg Gly Thr
            125                 130                 135

Ile Met Asp Thr Thr Val Asp Val Asp Lys Arg Val Met Glu Thr
            140                 145                 150

Asn Tyr Phe Gly Pro Val Ala Leu Thr Lys Ala Leu Leu Pro Ser
            155                 160                 165

Met Ile Lys Arg Arg Gln Gly His Ile Val Ala Ile Ser Ser Ile
            170                 175                 180

Gln Gly Lys Met Ser Ile Pro Phe Arg Ser Ala Tyr Ala Ala Ser
            185                 190                 195

Lys His Ala Thr Gln Ala Phe Phe Asp Cys Leu Arg Ala Glu Met
            200                 205                 210

Glu Gln Tyr Glu Ile Glu Val Thr Val Ile Ser Pro Gly Tyr Ile
            215                 220                 225

His Thr Asn Leu Ser Val Asn Ala Ile Thr Ala Asp Gly Ser Arg
            230                 235                 240

Tyr Gly Val Met Asp Thr Thr Thr Ala Gln Gly Arg Ser Pro Val
            245                 250                 255

Glu Val Ala Gln Asp Val Leu Ala Ala Val Gly Lys Lys Lys Lys
            260                 265                 270

Asp Val Ile Leu Ala Asp Leu Leu Pro Ser Leu Ala Val Tyr Leu
            275                 280                 285
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Arg Thr Leu Ala Pro Gly Leu Phe Phe Ser Leu Met Ala Ser Arg
290 295 300

Ala Arg Lys Glu Arg Lys Ser Lys Asn Ser
305 310

<210> 154
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 154
ggtgctaaac tggtgctctg tggc 24

<210> 155
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 155
cagggcaaga tgagcattcc 20

<210> 156
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 156
tcatactgtt ccatctcggc acgc 24

<210> 157
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 157
aatggtgggg ccctagaaga gctcatcaga gaactcaccg cttctcatgc 50

<210> 158
<211> 1771
<212> DNA
<213> Homo Sapien

<400> 158
cccacgcgtc cgctggtgtt agatcgagca accctctaaa agcagtttag 50

agtggtaaaa aaaaaaaaaa acacaccaaa cgctcgcagc cacaaaaggg 100

atgaaatttc ttctggacat cctcctgctt ctcccgttac tgatcgtctg 150

ctccctagag tccttcgtga agctttttat tcctaagagg agaaaatcag 200

tcaccggcga aatcgtgctg attacaggag ctgggcatgg aattgggaga 250

ctgactgcct atgaatttgc taaacttaaa agcaagctgg ttctctggga 300

tataaataag catggactgg aggaaacagc tgccaaatgc aagggactgg 350

gtgccaaggt tcataccttt gtggtagact gcagcaaccg agaagatatt 400

tacagctctg caaagaaggt gaaggcagaa attggagatg ttagtatttt 450

agtaaataat gctggtgtag tctatacatc agatttgttt gctacacaag 500

atcctcagat tgaaaagact tttgaagtta atgtacttgc acatttctgg 550

actacaaagg catttcttcc tgcaatgacg aagaataacc atggccatat 600

tgtcactgtg gcttcggcag ctggacatgt ctcggtcccc ttcttactgg 650

cttactgttc aagcaagttt gctgctgttg gatttcataa aactttgaca 700

gatgaactgg ctgccttaca aataactgga gtcaaaacaa catgtctgtg 750

tcctaatttc gtaaacactg gcttcatcaa aaatccaagt acaagtttgg 800

gacccactct ggaacctgag gaagtggtaa acaggctgat gcatgggatt 850

ctgactgagc agaagatgat ttttattcca tcttctatag ctttttaac 900

aacattggaa aggatccttc ctgagcgttt cctggcagtt ttaaaacgaa 950

aaatcagtgt taagtttgat gcagttattg gatataaaat gaaagcgcaa 1000

taagcaccta gttttctgaa aactgattta ccaggtttag gttgatgtca 1050

tctaatagtg ccagaatttt aatgtttgaa cttctgtttt ttctaattat 1100

ccccatttct tcaatatcat ttttgaggct ttggcagtct tcatttacta 1150

ccacttgttc tttagccaaa agctgattac atatgatata aacagagaaa 1200

tacctttaga ggtgacttta aggaaaatga agaaaaagaa ccaaaatgac 1250

tttattaaaa taatttccaa gattatttgt ggctcacctg aaggctttgc 1300

aaaatttgta ccataaccgt ttatttaaca tatattttta tttttgattg 1350

cacttaaatt ttgtataatt tgtgtttctt tttctgttct acataaaatc 1400

agaaacttca agctctctaa ataaaatgaa ggactatatc tagtggtatt 1450

tcacaatgaa tatcatgaac tctcaatggg taggtttcat cctacccatt 1500

gccactctgt ttcctgagag atacctcaca ttccaatgcc aaacatttct 1550

gcacagggaa gctagaggtg gatacacgtg ttgcaagtat aaaagcatca 1600

ctgggattta aggagaattg agagaatgta cccacaaatg gcagcaataa 1650

taaatggatc acacttaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1700

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1750

aaaaaaaaaa aaaaaaaaaa a 1771

<210> 159
<211> 300
<212> PRT
<213> Homo Sapien

<400> 159

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Met Lys Phe Leu Leu Asp Ile Leu Leu Leu Leu Pro Leu Leu Ile
  1               5                  10                  15

Val Cys Ser Leu Glu Ser Phe Val Lys Leu Phe Ile Pro Lys Arg
             20                  25                  30

Arg Lys Ser Val Thr Gly Glu Ile Val Leu Ile Thr Gly Ala Gly
             35                  40                  45

His Gly Ile Gly Arg Leu Thr Ala Tyr Glu Phe Ala Lys Leu Lys
             50                  55                  60

Ser Lys Leu Val Leu Trp Asp Ile Asn Lys His Gly Leu Glu Glu
             65                  70                  75

Thr Ala Ala Lys Cys Lys Gly Leu Gly Ala Lys Val His Thr Phe
             80                  85                  90

Val Val Asp Cys Ser Asn Arg Glu Asp Ile Tyr Ser Ser Ala Lys
             95                 100                 105

Lys Val Lys Ala Glu Ile Gly Asp Val Ser Ile Leu Val Asn Asn
            110                 115                 120

Ala Gly Val Val Tyr Thr Ser Asp Leu Phe Ala Thr Gln Asp Pro
            125                 130                 135

Gln Ile Glu Lys Thr Phe Glu Val Asn Val Leu Ala His Phe Trp
            140                 145                 150

Thr Thr Lys Ala Phe Leu Pro Ala Met Thr Lys Asn Asn His Gly
            155                 160                 165

His Ile Val Thr Val Ala Ser Ala Ala Gly His Val Ser Val Pro
            170                 175                 180

Phe Leu Leu Ala Tyr Cys Ser Ser Lys Phe Ala Ala Val Gly Phe
            185                 190                 195

His Lys Thr Leu Thr Asp Glu Leu Ala Ala Leu Gln Ile Thr Gly
            200                 205                 210

Val Lys Thr Thr Cys Leu Cys Pro Asn Phe Val Asn Thr Gly Phe
            215                 220                 225

Ile Lys Asn Pro Ser Thr Ser Leu Gly Pro Thr Leu Glu Pro Glu
            230                 235                 240

Glu Val Val Asn Arg Leu Met His Gly Ile Leu Thr Glu Gln Lys
            245                 250                 255

Met Ile Phe Ile Pro Ser Ser Ile Ala Phe Leu Thr Thr Leu Glu
            260                 265                 270
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Arg Ile Leu Pro Glu Arg Phe Leu Ala Val Leu Lys Arg Lys Ile
275 280 285

Ser Val Lys Phe Asp Ala Val Ile Gly Tyr Lys Met Lys Ala Gln
290 295 300

<210> 160
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 160
ggtgaaggca gaaattggag atg 23

<210> 161
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 161
atcccatgca tcagcctgtt tacc 24

<210> 162
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 162
gctggtgtag tctatacatc agatttgttt gctacacaag atcctcag 48

<210> 163
<211> 2076
<212> DNA
<213> Homo Sapien

<400> 163
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cgcccgcggc tcagggagga gcaccgactg cgccgcaccc tgagagatgg 100

ttggtgccat gtggaaggtg attgtttcgc tggtcctgtt gatgcctggc 150

ccctgtgatg ggctgtttcg ctccctatac agaagtgttt ccatgccacc 200

taagggagac tcaggacagc cattatttct cacccttac attgaagctg 250

ggaagatcca aaaaggaaga gaattgagtt tggtcggccc tttcccagga 300

ctgaacatga agagttatgc cggcttcctc accgtgaata agacttacaa 350

cagcaacctc ttcttctggt tcttcccagc tcagatacag ccagaagatg 400

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gtttttccag atatttcctg aatataaaaa taatgacttt tatgtcactg 700

gggagtctta tgcagggaaa tatgtgccag ccattgcaca cctcatccat 750

tccctcaacc ctgtgagaga ggtgaagatc aacctgaacg gaattgctat 800

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tggaagatct ttaaatctga cagtgaagtg gctggttaca tccggcaagc 1400

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tacaaaatta acatgagtac atgagtaaga attacattat ttaacttaaa 1750

ggatgaaagg tatggatgat gtgacactga gacaagatgt ataaatgaaa 1800

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tattatatat aaaagtaaaa aaaaaa 2076

<210> 164
<211> 476
<212> PRT
<213> Homo Sapien

<400> 164

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Met Val Gly Ala Met Trp Lys Val Ile Val Ser Leu Val Leu Leu
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Met Pro Gly Pro Cys Asp Gly Leu Phe Arg Ser Leu Tyr Arg Ser
             20                  25                  30

Val Ser Met Pro Pro Lys Gly Asp Ser Gly Gln Pro Leu Phe Leu
             35                  40                  45

Thr Pro Tyr Ile Glu Ala Gly Lys Ile Gln Lys Gly Arg Glu Leu
             50                  55                  60

Ser Leu Val Gly Pro Phe Pro Gly Leu Asn Met Lys Ser Tyr Ala
             65                  70                  75

Gly Phe Leu Thr Val Asn Lys Thr Tyr Asn Ser Asn Leu Phe Phe
             80                  85                  90

Trp Phe Phe Pro Ala Gln Ile Gln Pro Glu Asp Ala Pro Val Val
             95                 100                 105

Leu Trp Leu Gln Gly Gly Pro Gly Gly Ser Ser Met Phe Gly Leu
            110                 115                 120

Phe Val Glu His Gly Pro Tyr Val Val Thr Ser Asn Met Thr Leu
            125                 130                 135

Arg Asp Arg Asp Phe Pro Trp Thr Thr Thr Leu Ser Met Leu Tyr
            140                 145                 150

Ile Asp Asn Pro Val Gly Thr Gly Phe Ser Phe Thr Asp Asp Thr
            155                 160                 165

His Gly Tyr Ala Val Asn Glu Asp Asp Val Ala Arg Asp Leu Tyr
            170                 175                 180

Ser Ala Leu Ile Gln Phe Phe Gln Ile Phe Pro Glu Tyr Lys Asn
            185                 190                 195

Asn Asp Phe Tyr Val Thr Gly Glu Ser Tyr Ala Gly Lys Tyr Val
            200                 205                 210

Pro Ala Ile Ala His Leu Ile His Ser Leu Asn Pro Val Arg Glu
            215                 220                 225

Val Lys Ile Asn Leu Asn Gly Ile Ala Ile Gly Asp Gly Tyr Ser
            230                 235                 240

Asp Pro Glu Ser Ile Ile Gly Gly Tyr Ala Glu Phe Leu Tyr Gln
            245                 250                 255

Ile Gly Leu Leu Asp Glu Lys Gln Lys Lys Tyr Phe Gln Lys Gln
            260                 265                 270
```

Cys His Glu Cys Ile Glu His Ile Arg Lys Gln Asn Trp Phe Glu
275 280 285

Ala Phe Glu Ile Leu Asp Lys Leu Leu Asp Gly Asp Leu Thr Ser
290 295 300

Asp Pro Ser Tyr Phe Gln Asn Val Thr Gly Cys Ser Asn Tyr Tyr
305 310 315

Asn Phe Leu Arg Cys Thr Glu Pro Glu Asp Gln Leu Tyr Tyr Val
320 325 330

Lys Phe Leu Ser Leu Pro Glu Val Arg Gln Ala Ile His Val Gly
335 340 345

Asn Gln Thr Phe Asn Asp Gly Thr Ile Val Glu Lys Tyr Leu Arg
350 355 360

Glu Asp Thr Val Gln Ser Val Lys Pro Trp Leu Thr Glu Ile Met
365 370 375

Asn Asn Tyr Lys Val Leu Ile Tyr Asn Gly Gln Leu Asp Ile Ile
380 385 390

Val Ala Ala Ala Leu Thr Glu Arg Ser Leu Met Gly Met Asp Trp
395 400 405

Lys Gly Ser Gln Glu Tyr Lys Lys Ala Glu Lys Lys Val Trp Lys
410 415 420

Ile Phe Lys Ser Asp Ser Glu Val Ala Gly Tyr Ile Arg Gln Ala
425 430 435

Gly Asp Phe His Gln Val Ile Ile Arg Gly Gly Gly His Ile Leu
440 445 450

Pro Tyr Asp Gln Pro Leu Arg Ala Phe Asp Met Ile Asn Arg Phe
455 460 465

Ile Tyr Gly Lys Gly Trp Asp Pro Tyr Val Gly
470 475

<210> 165
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 165
ttccatgcca cctaagggag actc 24

<210> 166
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 166
tggatgaggt gtgcaatggc tggc 24

<210> 167
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 167
agctctcaga ggctggtcat aggg 24

<210> 168
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 168
gtcggccctt tcccaggact gaacatgaag agttatgccg gcttcctcac 50

<210> 169
<211> 2477
<212> DNA
<213> Homo Sapien

<400> 169
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tggctacaac atttttccct ttcctaacaa gttctaacag ctgttctaac 100

agctagtgat caggggttct tcttgctgga gaagaaaggg ctgagggcag 150

agcagggcac tctcactcag ggtgaccagc tccttgcctc tctgtggata 200

acagagcatg agaaagtgaa gagatgcagc ggagtgaggt gatggaagtc 250

taaaatagga aggaattttg tgtgcaatat cagactctgg gagcagttga 300

cctggagagc ctgggggagg gcctgcctaa caagctttca aaaaacagga 350

gcgacttcca ctgggctggg ataagacgtg ccggtaggat agggaagact 400

gggtttagtc ctaatatcaa attgactggc tgggtgaact tcaacagcct 450

tttaacctct ctgggagatg aaaacgatgg cttaaggggc cagaaataga 500

gatgctttgt aaaataaaat tttaaaaaaa gcaagtattt tatagcataa 550

aggctagaga ccaaaataga taacaggatt ccctgaacat tcctaagagg 600

gagaaagtat gttaaaaata gaaaaaccaa aatgcagaag gaggagactc 650

acagagctaa accaggatgg ggaccctggg tcaggccagc ctctttgctc 700

ctcccggaaa ttatttttgg tctgaccact ctgccttgtg ttttgcagaa 750

tcatgtgagg gccaaccggg gaaggtggag cagatgagca cacacaggag 800

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ggcaacctga ccatccaggt ggctcataag acagggccag aagaggacaa 1100

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ccctcaccaa caatgtcaac aagctgctca tcattgacta ctctgagaac 1200

cgcctgctgg cctgtgggag cctctaccag ggggtctgca agctgctgcg 1250

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tttgtgactt agcttctagc tacttcctcc agccatcagt cattgggtat 2400

gtaaggaatg caagcgtatt tcaatatttc ccaaacttta agaaaaaact 2450

ttaagaaggt acatctgcaa aagcaaa 2477

<210> 170
<211> 552
<212> PRT
<213> Homo Sapien

<400> 170

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Met Gly Thr Leu Gly Gln Ala Ser Leu Phe Ala Pro Pro Gly Asn
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Tyr Phe Trp Ser Asp His Ser Ala Leu Cys Phe Ala Glu Ser Cys
             20                  25                  30

Glu Gly Gln Pro Gly Lys Val Glu Gln Met Ser Thr His Arg Ser
             35                  40                  45

Arg Leu Leu Thr Ala Ala Pro Leu Ser Met Glu Gln Arg Gln Pro
             50                  55                  60

Trp Pro Arg Ala Leu Glu Val Asp Ser Arg Ser Val Val Leu Leu
             65                  70                  75

Ser Val Val Trp Val Leu Leu Ala Pro Pro Ala Ala Gly Met Pro
             80                  85                  90

Gln Phe Ser Thr Phe His Ser Glu Asn Arg Asp Trp Thr Phe Asn
             95                 100                 105

His Leu Thr Val His Gln Gly Thr Gly Ala Val Tyr Val Gly Ala
            110                 115                 120

Ile Asn Arg Val Tyr Lys Leu Thr Gly Asn Leu Thr Ile Gln Val
            125                 130                 135

Ala His Lys Thr Gly Pro Glu Glu Asp Asn Lys Ser Arg Tyr Pro
            140                 145                 150

Pro Leu Ile Val Gln Pro Cys Ser Glu Val Leu Thr Leu Thr Asn
            155                 160                 165

Asn Val Asn Lys Leu Leu Ile Ile Asp Tyr Ser Glu Asn Arg Leu
            170                 175                 180

Leu Ala Cys Gly Ser Leu Tyr Gln Gly Val Cys Lys Leu Leu Arg
            185                 190                 195

Leu Asp Asp Leu Phe Ile Leu Val Glu Pro Ser His Lys Lys Glu
            200                 205                 210

His Tyr Leu Ser Ser Val Asn Lys Thr Gly Thr Met Tyr Gly Val
            215                 220                 225

Ile Val Arg Ser Glu Gly Glu Asp Gly Lys Leu Phe Ile Gly Thr
            230                 235                 240

Ala Val Asp Gly Lys Gln Asp Tyr Phe Pro Thr Leu Ser Ser Arg
            245                 250                 255

Lys Leu Pro Arg Asp Pro Glu Ser Ser Ala Met Leu Asp Tyr Glu
            260                 265                 270
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Leu His Ser Asp Phe Val Ser Ser Leu Ile Lys Ile Pro Ser Asp
275 280 285

Thr Leu Ala Leu Val Ser His Phe Asp Ile Phe Tyr Ile Tyr Gly
290 295 300

Phe Ala Ser Gly Gly Phe Val Tyr Phe Leu Thr Val Gln Pro Glu
305 310 315

Thr Pro Glu Gly Val Ala Ile Asn Ser Ala Gly Asp Leu Phe Tyr
320 325 330

Thr Ser Arg Ile Val Arg Leu Cys Lys Asp Asp Pro Lys Phe His
335 340 345

Ser Tyr Val Ser Leu Pro Phe Gly Cys Thr Arg Ala Gly Val Glu
350 355 360

Tyr Arg Leu Leu Gln Ala Ala Tyr Leu Ala Lys Pro Gly Asp Ser
365 370 375

Leu Ala Gln Ala Phe Asn Ile Thr Ser Gln Asp Asp Val Leu Phe
380 385 390

Ala Ile Phe Ser Lys Gly Gln Lys Gln Tyr His His Pro Pro Asp
395 400 405

Asp Ser Ala Leu Cys Ala Phe Pro Ile Arg Ala Ile Asn Leu Gln
410 415 420

Ile Lys Glu Arg Leu Gln Ser Cys Tyr Gln Gly Glu Gly Asn Leu
425 430 435

Glu Leu Asn Trp Leu Leu Gly Lys Asp Val Gln Cys Thr Lys Ala
440 445 450

Pro Val Pro Ile Asp Asp Asn Phe Cys Gly Leu Asp Ile Asn Gln
455 460 465

Pro Leu Gly Gly Ser Thr Pro Val Glu Gly Leu Thr Leu Tyr Thr
470 475 480

Thr Ser Arg Asp Arg Met Thr Ser Val Ala Ser Tyr Val Tyr Asn
485 490 495

Gly Tyr Ser Val Val Phe Val Gly Thr Lys Ser Gly Lys Leu Lys
500 505 510

Lys Val Arg Val Tyr Glu Phe Arg Cys Ser Asn Ala Ile His Leu
515 520 525

Leu Ser Lys Glu Ser Leu Leu Glu Gly Ser Tyr Trp Trp Arg Phe
530 535 540

Asn Tyr Arg Gln Leu Tyr Phe Leu Gly Glu Gln Arg
545 550

<210> 171
<211> 20
<212> DNA
<213> Artificial Sequence

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<223> Synthetic Oligonucleotide Probe

<400> 171
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<210> 172
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 172
cttctgccct ttggagaaga tggc 24

<210> 173
<211> 43
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 173
ggactcactg gcccaggcct tcaatatcac cagccaggac gat 43

<210> 174
<211> 3106
<212> DNA
<213> Homo Sapien

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<221> unsure
<222> 1683
<223> unknown base

<400> 174
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gcaggctgga ctggagcacc ctggtccctc tgcggctccg ccatcgacag 200

ctggggctgc aggccaaggg ctggaacttc atgctggagg attccacctt 250

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ggagggaccg cctgctgaag atgaaggcct gtggcttgaa caccctcacc 350

acctatgttc cgtggaacct gcatgagcca gaaagaggca aatttgactt 400

ctctgggaac ctggacctgg aggccttcgt cctgatggcc gcagagatcg 450

ggctgtgggt gattctgcgt ccaggcccct acatctgcag tgagatggac 500

ctcgggggct tgcccagctg gctactccaa gaccctggca tgaggctgag 550

gacaacttac aagggcttca ccgaagcagt ggacctttat tttgaccacc 600

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gccgtgcagg tggagaatga atatggttcc tataataaag accccgcata 700

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catgtctgca catccaggga ggaggacaga aggcccagct cagtggcccc 2950

cgctccccac cccccacgcc cgaacagcag gggcagagca gccctccttc 3000

gaagtgtgtc caagtccgca tttgagcctt gttctggggc ccagcccaac 3050

acctggcttg ggctcactgt cctgagttgc agtaaagcta taaccttgaa 3100

tcacaa 3106

<210> 175
<211> 636
<212> PRT
<213> Homo Sapien

<220>
<221> unsure
<222> 539
<223> unknown amino acid

<400> 175

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1 5 10 15

Leu Leu Leu Leu Val Val Leu Gly Phe Leu Val Leu Arg Arg Leu
20 25 30

Asp Trp Ser Thr Leu Val Pro Leu Arg Leu Arg His Arg Gln Leu
35 40 45

Gly Leu Gln Ala Lys Gly Trp Asn Phe Met Leu Glu Asp Ser Thr
50 55 60

Phe Trp Ile Phe Gly Gly Ser Ile His Tyr Phe Arg Val Pro Arg
65 70 75

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Glu Tyr Trp Arg Asp Arg Leu Leu Lys Met Lys Ala Cys Gly Leu
 80                  85                  90

Asn Thr Leu Thr Thr Tyr Val Pro Trp Asn Leu His Glu Pro Glu
 95                 100                 105

Arg Gly Lys Phe Asp Phe Ser Gly Asn Leu Asp Leu Glu Ala Phe
110                 115                 120

Val Leu Met Ala Ala Glu Ile Gly Leu Trp Val Ile Leu Arg Pro
125                 130                 135

Gly Pro Tyr Ile Cys Ser Glu Met Asp Leu Gly Gly Leu Pro Ser
140                 145                 150

Trp Leu Leu Gln Asp Pro Gly Met Arg Leu Arg Thr Thr Tyr Lys
155                 160                 165

Gly Phe Thr Glu Ala Val Asp Leu Tyr Phe Asp His Leu Met Ser
170                 175                 180

Arg Val Val Pro Leu Gln Tyr Lys Arg Gly Gly Pro Ile Ile Ala
185                 190                 195

Val Gln Val Glu Asn Glu Tyr Gly Ser Tyr Asn Lys Asp Pro Ala
200                 205                 210

Tyr Met Pro Tyr Val Lys Lys Ala Leu Glu Asp Arg Gly Ile Val
215                 220                 225

Glu Leu Leu Leu Thr Ser Asp Asn Lys Asp Gly Leu Ser Lys Gly
230                 235                 240

Ile Val Gln Gly Val Leu Ala Thr Ile Asn Leu Gln Ser Thr His
245                 250                 255

Glu Leu Gln Leu Leu Thr Thr Phe Leu Phe Asn Val Gln Gly Thr
260                 265                 270

Gln Pro Lys Met Val Met Glu Tyr Trp Thr Gly Trp Phe Asp Ser
275                 280                 285

Trp Gly Gly Pro His Asn Ile Leu Asp Ser Ser Glu Val Leu Lys
290                 295                 300

Thr Val Ser Ala Ile Val Asp Ala Gly Ser Ser Ile Asn Leu Tyr
305                 310                 315

Met Phe His Gly Gly Thr Asn Phe Gly Phe Met Asn Gly Ala Met
320                 325                 330

His Phe His Asp Tyr Lys Ser Asp Val Thr Ser Tyr Asp Tyr Asp
335                 340                 345

Ala Val Leu Thr Glu Ala Gly Asp Tyr Thr Ala Lys Tyr Met Lys
350                 355                 360

Leu Arg Asp Phe Phe Gly Ser Ile Ser Gly Ile Pro Leu Pro Pro
365                 370                 375

Pro Pro Asp Leu Leu Pro Lys Met Pro Tyr Glu Pro Leu Thr Pro
380                 385                 390
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Val Leu Tyr Leu Ser Leu Trp Asp Ala Leu Lys Tyr Leu Gly Glu
395 400 405

Pro Ile Lys Ser Glu Lys Pro Ile Asn Met Glu Asn Leu Pro Val
410 415 420

Asn Gly Gly Asn Gly Gln Ser Phe Gly Tyr Ile Leu Tyr Glu Thr
425 430 435

Ser Ile Thr Ser Ser Gly Ile Leu Ser Gly His Val His Asp Arg
440 445 450

Gly Gln Val Phe Val Asn Thr Val Ser Ile Gly Phe Leu Asp Tyr
455 460 465

Lys Thr Thr Lys Ile Ala Val Pro Leu Ile Gln Gly Tyr Thr Val
470 475 480

Leu Arg Ile Leu Val Glu Asn Arg Gly Arg Val Asn Tyr Gly Glu
485 490 495

Asn Ile Asp Asp Gln Arg Lys Gly Leu Ile Gly Asn Leu Tyr Leu
500 505 510

Asn Asp Ser Pro Leu Lys Asn Phe Arg Ile Tyr Ser Leu Asp Met
515 520 525

Lys Lys Ser Phe Phe Gln Arg Phe Gly Leu Asp Lys Trp Xaa Ser
530 535 540

Leu Pro Glu Thr Pro Thr Leu Pro Ala Phe Phe Leu Gly Ser Leu
545 550 555

Ser Ile Ser Ser Thr Pro Cys Asp Thr Phe Leu Lys Leu Glu Gly
560 565 570

Trp Glu Lys Gly Val Val Phe Ile Asn Gly Gln Asn Leu Gly Arg
575 580 585

Tyr Trp Asn Ile Gly Pro Gln Lys Thr Leu Tyr Leu Pro Gly Pro
590 595 600

Trp Leu Ser Ser Gly Ile Asn Gln Val Ile Val Phe Glu Glu Thr
605 610 615

Met Ala Gly Pro Ala Leu Gln Phe Thr Glu Thr Pro His Leu Gly
620 625 630

Arg Asn Gln Tyr Ile Lys
635

<210> 176
<211> 2505
<212> DNA
<213> Homo Sapien

<400> 176
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ggtcccagga ccctggtgag ggttctctac ttggccttcg gtgggggtca 100

agacgcaggc acctacgcca aaggggagca aagccgggct cggcccgagg 150

ccccccaggac ctccatctcc caatgttgga ggaatccgac acgtgacggt 200
ctgtccgccg tctcagacta gaggagcgct gtaaacgcca tggctcccaa 250
gaagctgtcc tgccttcgtt ccctgctgct gccgctcagc ctgacgctac 300
tgctgcccca ggcagacact cggtcgttcg tagtggatag gggtcatgac 350
cggtttctcc tagacggggc cccgttccgc tatgtgtctg gcagcctgca 400
ctactttcgg gtaccgcggg tgctttgggc cgaccggctt ttgaagatgc 450
gatggagcgg cctcaacgcc atacagtttt atgtgccctg gaactaccac 500
gagccacagc ctggggtcta taactttaat ggcagccggg acctcattgc 550
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tttatcacaa tgggggcaac atcattagca ttcaggtgga gaatgaatat 800
ggtagctaca gagcctgtga cttcagctac atgaggcact tggctgggct 850
cttccgtgca ctgctaggag aaaagatctt gctcttcacc acagatgggc 900
ctgaaggact caagtgtggc tccctccggg gactctatac cactgtagat 950
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tgaaccccat gggccattgg taaactctga gtactacaca ggctggctgg 1050
attactgggg ccagaatcac tccacacggt ctgtgtcagc tgtaaccaaa 1100
ggactagaga acatgctcaa gttgggagcc agtgtgaaca tgtacatgtt 1150
ccatggaggt accaactttg gatattggaa tggtgccgat aagaagggac 1200
gcttccttcc gattactacc agctatgact atgatgcacc tatatctgaa 1250
gcaggggacc ccacacctaa gctttttgct cttcgagatg tcatcagcaa 1300
gttccaggaa gttcctttgg gacctttacc tcccccgagc cccaagatga 1350
tgcttggacc tgtgactctg cacctggttg ggcatttact ggctttccta 1400
gacttgcttt gcccccgtgg gcccattcat tcaatcttgc caatgacctt 1450
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cccataccat ttttgagcca acaccattct gggtgccaaa taatggagtc 1550
catgaccgtg cctatgtgat ggtggatggg gtgttccagg gtgttgtgga 1600
gcgaaatatg agagacaaac tatttttgac ggggaaactg gggtccaaac 1650
tggatatctt ggtggagaac atggggaggc tcagctttgg gtctaacagc 1700

agtgacttca agggcctgtt gaagccacca attctggggc aaacaatcct 1750

tacccagtgg atgatgttcc ctctgaaaat tgataacctt gtgaagtggt 1800

ggtttcccct ccagttgcca aaatggccat atcctcaagc tccttctggc 1850

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agcctatcct caatagcact agtactttgc acaggacaca tatcaattcc 2150

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gggaggctga gacgggtgga ttacctgagg tcaggacttc aagaccagcc 2300

tggccaacat ggtgaaaccc cgtctccact aaaaatacaa aaattagccg 2350

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accactgcac tccagcctgg ctgacagtga gacactccat ctcaaaaaaa 2500

aaaaa 2505

<210> 177
<211> 654
<212> PRT
<213> Homo Sapien

<400> 177

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Leu	Ser	Leu	Thr	Leu	Leu	Leu	Pro	Gln	Ala	Asp	Thr	Arg	Ser	Phe
			20					25					30	
Val	Val	Asp	Arg	Gly	His	Asp	Arg	Phe	Leu	Leu	Asp	Gly	Ala	Pro
			35					40					45	
Phe	Arg	Tyr	Val	Ser	Gly	Ser	Leu	His	Tyr	Phe	Arg	Val	Pro	Arg
			50					55					60	
Val	Leu	Trp	Ala	Asp	Arg	Leu	Leu	Lys	Met	Arg	Trp	Ser	Gly	Leu
			65					70					75	
Asn	Ala	Ile	Gln	Phe	Tyr	Val	Pro	Trp	Asn	Tyr	His	Glu	Pro	Gln
			80					85					90	
Pro	Gly	Val	Tyr	Asn	Phe	Asn	Gly	Ser	Arg	Asp	Leu	Ile	Ala	Phe
			95					100					105	
Leu	Asn	Glu	Ala	Ala	Leu	Ala	Asn	Leu	Leu	Val	Ile	Leu	Arg	Pro
			110					115					120	

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Gly Pro Tyr Ile Cys Ala Glu Trp Glu Met Gly Gly Leu Pro Ser
                125                 130                 135

Trp Leu Leu Arg Lys Pro Glu Ile His Leu Arg Thr Ser Asp Pro
                140                 145                 150

Asp Phe Leu Ala Ala Val Asp Ser Trp Phe Lys Val Leu Leu Pro
                155                 160                 165

Lys Ile Tyr Pro Trp Leu Tyr His Asn Gly Gly Asn Ile Ile Ser
                170                 175                 180

Ile Gln Val Glu Asn Glu Tyr Gly Ser Tyr Arg Ala Cys Asp Phe
                185                 190                 195

Ser Tyr Met Arg His Leu Ala Gly Leu Phe Arg Ala Leu Leu Gly
                200                 205                 210

Glu Lys Ile Leu Leu Phe Thr Thr Asp Gly Pro Glu Gly Leu Lys
                215                 220                 225

Cys Gly Ser Leu Arg Gly Leu Tyr Thr Thr Val Asp Phe Gly Pro
                230                 235                 240

Ala Asp Asn Met Thr Lys Ile Phe Thr Leu Leu Arg Lys Tyr Glu
                245                 250                 255

Pro His Gly Pro Leu Val Asn Ser Glu Tyr Tyr Thr Gly Trp Leu
                260                 265                 270

Asp Tyr Trp Gly Gln Asn His Ser Thr Arg Ser Val Ser Ala Val
                275                 280                 285

Thr Lys Gly Leu Glu Asn Met Leu Lys Leu Gly Ala Ser Val Asn
                290                 295                 300

Met Tyr Met Phe His Gly Gly Thr Asn Phe Gly Tyr Trp Asn Gly
                305                 310                 315

Ala Asp Lys Lys Gly Arg Phe Leu Pro Ile Thr Thr Ser Tyr Asp
                320                 325                 330

Tyr Asp Ala Pro Ile Ser Glu Ala Gly Asp Pro Thr Pro Lys Leu
                335                 340                 345

Phe Ala Leu Arg Asp Val Ile Ser Lys Phe Gln Glu Val Pro Leu
                350                 355                 360

Gly Pro Leu Pro Pro Pro Ser Pro Lys Met Met Leu Gly Pro Val
                365                 370                 375

Thr Leu His Leu Val Gly His Leu Leu Ala Phe Leu Asp Leu Leu
                380                 385                 390

Cys Pro Arg Gly Pro Ile His Ser Ile Leu Pro Met Thr Phe Glu
                395                 400                 405

Ala Val Lys Gln Asp His Gly Phe Met Leu Tyr Arg Thr Tyr Met
                410                 415                 420

Thr His Thr Ile Phe Glu Pro Thr Pro Phe Trp Val Pro Asn Asn
                425                 430                 435
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Gly Val His Asp Arg Ala Tyr Val Met Val Asp Gly Val Phe Gln
440 445 450

Gly Val Val Glu Arg Asn Met Arg Asp Lys Leu Phe Leu Thr Gly
455 460 465

Lys Leu Gly Ser Lys Leu Asp Ile Leu Val Glu Asn Met Gly Arg
470 475 480

Leu Ser Phe Gly Ser Asn Ser Ser Asp Phe Lys Gly Leu Leu Lys
485 490 495

Pro Pro Ile Leu Gly Gln Thr Ile Leu Thr Gln Trp Met Met Phe
500 505 510

Pro Leu Lys Ile Asp Asn Leu Val Lys Trp Trp Phe Pro Leu Gln
515 520 525

Leu Pro Lys Trp Pro Tyr Pro Gln Ala Pro Ser Gly Pro Thr Phe
530 535 540

Tyr Ser Lys Thr Phe Pro Ile Leu Gly Ser Val Gly Asp Thr Phe
545 550 555

Leu Tyr Leu Pro Gly Trp Thr Lys Gly Gln Val Trp Ile Asn Gly
560 565 570

Phe Asn Leu Gly Arg Tyr Trp Thr Lys Gln Gly Pro Gln Gln Thr
575 580 585

Leu Tyr Val Pro Arg Phe Leu Leu Phe Pro Arg Gly Ala Leu Asn
590 595 600

Lys Ile Thr Leu Leu Glu Leu Glu Asp Val Pro Leu Gln Pro Gln
605 610 615

Val Gln Phe Leu Asp Lys Pro Ile Leu Asn Ser Thr Ser Thr Leu
620 625 630

His Arg Thr His Ile Asn Ser Leu Ser Ala Asp Thr Leu Ser Ala
635 640 645

Ser Glu Pro Met Glu Leu Ser Gly His
650

<210> 178
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 178
tggctactcc aagaccctgg catg 24

<210> 179
<211> 24
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 179
tggacaaatc cccttgctca gccc 24

<210> 180
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 180
gggcttcacc gaagcagtgg acctttattt tgaccacctg atgtccaggg 50

<210> 181
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 181
ccagctatga ctatgatgca cc 22

<210> 182
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 182
tggcacccag aatggtgttg gctc 24

<210> 183
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 183
cgagatgtca tcagcaagtt ccaggaagtt cctttgggac ctttacctcc 50

<210> 184
<211> 1947
<212> DNA
<213> Homo Sapien

<400> 184
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gtatttgagt gcacccacaa tatggcttac atgttgaaaa agcttctcat 100

cagttacata tccattattt gtgtttatgg ctttatctgc ctctacactc 150

tcttctggtt attcaggata cctttgaagg aatattcttt cgaaaaagtc 200

agagaagaga gcagttttag tgacattcca gatgtcaaaa acgattttgc 250

gttccttctt cacatggtag accagtatga ccagctatat tccaagcgtt 300

ttggtgtgtt cttgtcagaa gttagtgaaa ataaacttag ggaaattagt 350

ttgaaccatg agtggacatt tgaaaaactc aggcagcaca tttcacgcaa 400

cgcccaggac aagcaggagt tgcatctgtt catgctgtcg ggggtgcccg 450

atgctgtctt tgacctcaca gacctggatg tgctaaagct tgaactaatt 500

ccagaagcta aaattcctgc taagatttct caaatgacta acctccaaga 550

gctccacctc tgccactgcc ctgcaaaagt tgaacagact gcttttagct 600

ttcttcgcga tcacttgaga tgccttcacg tgaagttcac tgatgtggct 650

gaaattcctg cctgggtgta tttgctcaaa aaccttcgag agttgtactt 700

aataggcaat ttgaactctg aaaacaataa gatgatagga cttgaatctc 750

tccgagagtt gcggcacctt aagattctcc acgtgaagag caatttgacc 800

aaagttccct ccaacattac agatgtggct ccacatctta caaagttagt 850

cattcataat gacggcacta aactcttggt actgaacagc cttaagaaaa 900

tgatgaatgt cgctgagctg gaactccaga actgtgagct agagagaatc 950

ccacatgcta ttttcagcct ctctaattta caggaactgg atttaaagtc 1000

caataacatt cgcacaattg aggaaatcat cagtttccag catttaaaac 1050

gactgacttg tttaaaatta tggcataaca aaattgttac tattcctccc 1100

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gctcgaatcc ttaccagtgg cagtatttag tttacagaaa ctcagatgct 1200

tagatgtgag ctacaacaac atttcaatga ttccaataga aataggattg 1250

cttcagaacc tgcagcattt gcatatcact gggaacaaag tggacattct 1300

gccaaaacaa ttgtttaaat gcataaagtt gaggactttg aatctgggac 1350

agaactgcat cacctcactc ccagagaaag ttggtcagct ctcccagctc 1400

actcagctgg agctgaaggg gaactgcttg gaccgcctgc cagcccagct 1450

gggccagtgt cggatgctca agaaaagcgg gcttgttgtg gaagatcacc 1500

tttttgatac cctgccactc gaagtcaaag aggcattgaa tcaagacata 1550

aatattccct ttgcaaatgg gatttaaact aagataatat atgcacagtg 1600

atgtgcagga acaacttcct agattgcaag tgctcacgta caagttatta 1650

caagataatg cattttagga gtagatacat cttttaaaat aaaacagaga 1700

ggatgcatag aaggctgata gaagacataa ctgaatgttc aatgtttgta 1750

gggttttaag tcattcattt ccaaatcatt ttttttttc ttttggggaa 1800

agggaaggaa aaattataat cactaatctt ggttcttttt aaattgtttg 1850

taacttggat gctgccgcta ctgaatgttt acaaattgct tgcctgctaa 1900

agtaaatgat taaattgaca ttttcttact aaaaaaaaaa aaaaaaa 1947

<210> 185
<211> 501
<212> PRT
<213> Homo Sapien

<400> 185

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Met Ala Tyr Met Leu Lys Lys Leu Leu Ile Ser Tyr Ile Ser Ile
  1               5                  10                  15

Ile Cys Val Tyr Gly Phe Ile Cys Leu Tyr Thr Leu Phe Trp Leu
             20                  25                  30

Phe Arg Ile Pro Leu Lys Glu Tyr Ser Phe Glu Lys Val Arg Glu
             35                  40                  45

Glu Ser Ser Phe Ser Asp Ile Pro Asp Val Lys Asn Asp Phe Ala
             50                  55                  60

Phe Leu Leu His Met Val Asp Gln Tyr Asp Gln Leu Tyr Ser Lys
             65                  70                  75

Arg Phe Gly Val Phe Leu Ser Glu Val Ser Glu Asn Lys Leu Arg
             80                  85                  90

Glu Ile Ser Leu Asn His Glu Trp Thr Phe Glu Lys Leu Arg Gln
             95                 100                 105

His Ile Ser Arg Asn Ala Gln Asp Lys Gln Glu Leu His Leu Phe
            110                 115                 120

Met Leu Ser Gly Val Pro Asp Ala Val Phe Asp Leu Thr Asp Leu
            125                 130                 135

Asp Val Leu Lys Leu Glu Leu Ile Pro Glu Ala Lys Ile Pro Ala
            140                 145                 150

Lys Ile Ser Gln Met Thr Asn Leu Gln Glu Leu His Leu Cys His
            155                 160                 165

Cys Pro Ala Lys Val Glu Gln Thr Ala Phe Ser Phe Leu Arg Asp
            170                 175                 180

His Leu Arg Cys Leu His Val Lys Phe Thr Asp Val Ala Glu Ile
            185                 190                 195

Pro Ala Trp Val Tyr Leu Leu Lys Asn Leu Arg Glu Leu Tyr Leu
            200                 205                 210

Ile Gly Asn Leu Asn Ser Glu Asn Asn Lys Met Ile Gly Leu Glu
            215                 220                 225

Ser Leu Arg Glu Leu Arg His Leu Lys Ile Leu His Val Lys Ser
            230                 235                 240

Asn Leu Thr Lys Val Pro Ser Asn Ile Thr Asp Val Ala Pro His
            245                 250                 255
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Leu Thr Lys Leu Val Ile His Asn Asp Gly Thr Lys Leu Leu Val
260 265 270

Leu Asn Ser Leu Lys Lys Met Met Asn Val Ala Glu Leu Glu Leu
275 280 285

Gln Asn Cys Glu Leu Glu Arg Ile Pro His Ala Ile Phe Ser Leu
290 295 300

Ser Asn Leu Gln Glu Leu Asp Leu Lys Ser Asn Asn Ile Arg Thr
305 310 315

Ile Glu Glu Ile Ile Ser Phe Gln His Leu Lys Arg Leu Thr Cys
320 325 330

Leu Lys Leu Trp His Asn Lys Ile Val Thr Ile Pro Pro Ser Ile
335 340 345

Thr His Val Lys Asn Leu Glu Ser Leu Tyr Phe Ser Asn Asn Lys
350 355 360

Leu Glu Ser Leu Pro Val Ala Val Phe Ser Leu Gln Lys Leu Arg
365 370 375

Cys Leu Asp Val Ser Tyr Asn Asn Ile Ser Met Ile Pro Ile Glu
380 385 390

Ile Gly Leu Leu Gln Asn Leu Gln His Leu His Ile Thr Gly Asn
395 400 405

Lys Val Asp Ile Leu Pro Lys Gln Leu Phe Lys Cys Ile Lys Leu
410 415 420

Arg Thr Leu Asn Leu Gly Gln Asn Cys Ile Thr Ser Leu Pro Glu
425 430 435

Lys Val Gly Gln Leu Ser Gln Leu Thr Gln Leu Glu Leu Lys Gly
440 445 450

Asn Cys Leu Asp Arg Leu Pro Ala Gln Leu Gly Gln Cys Arg Met
455 460 465

Leu Lys Lys Ser Gly Leu Val Val Glu Asp His Leu Phe Asp Thr
470 475 480

Leu Pro Leu Glu Val Lys Glu Ala Leu Asn Gln Asp Ile Asn Ile
485 490 495

Pro Phe Ala Asn Gly Ile
500

<210> 186
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 186
cctccctcta ttacccatgt c 21

<210> 187
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 187
gaccaacttt ctctgggagt gagg 24

<210> 188
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 188
gtcactttat ttctctaaca acaagctcga atccttacca gtggcag 47

<210> 189
<211> 2917
<212> DNA
<213> Homo Sapien

<400> 189
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tgacaaactg actttttta tttctttttt tccatctctg ggccagcttg 100

ggatcctagg ccgccctggg aagacatttg tgttttacac acataaggat 150

ctgtgtttgg ggtttcttct tcctcccctg acattggcat tgcttagtgg 200

ttgtgtgggg agggagacca cgtgggctca gtgcttgctt gcacttatct 250

gcctaggtac atcgaagtct tttgacctcc atacagtgat tatgcctgtc 300

atcgctggtg gtatcctggc ggccttgctc ctgctgatag ttgtcgtgct 350

ctgtctttac ttcaaaatac acaacgcgct aaaagctgca aaggaacctg 400

aagctgtggc tgtaaaaaat cacaacccag acaaggtgtg gtgggccaag 450

aacagccagg ccaaaaccat tgccacggag tcttgtcctg ccctgcagtg 500

ctgtgaagga tatagaatgt gtgccagttt tgattccctg ccaccttgct 550

gttgcgacat aaatgagggc ctctgagtta ggaaaggctc ccttctcaaa 600

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gtgcaggcac agaagaaagg cacagctccc catcagtttc atggaaaata 700

actcagtgcc tgctgggaac cagctgctgg agatccctac agagagcttc 750

cactgggggc aacccttcca ggaaggagtt ggggagagag aaccctcact 800

gtggggaatg ctgataaacc agtcacacag ctgctctatt ctcacacaaa 850

tctacccctt gcgtggctgg aactgacgtt tccctggagg tgtccagaaa 900

gctgatgtaa cacagagcct ataaaagctg tcggtcctta aggctgccca 950

gcgccttgcc aaaatggagc ttgtaagaag gctcatgcca ttgaccctct 1000

taattctctc ctgtttggcg gagctgacaa tggcggaggc tgaaggcaat 1050

gcaagctgca cagtcagtct agggggtgcc aatatggcag agacccacaa 1100

agccatgatc ctgcaactca atcccagtga gaactgcacc tggacaatag 1150

aaagaccaga aaacaaaagc atcagaatta tcttttccta tgtccagctt 1200

gatccagatg gaagctgtga aagtgaaaac attaaagtct ttgacggaac 1250

ctccagcaat gggcctctgc tagggcaagt ctgcagtaaa aacgactatg 1300

ttcctgtatt tgaatcatca tccagtacat tgacgtttca aatagttact 1350

gactcagcaa gaattcaaag aactgtcttt gtcttctact acttcttctc 1400

tcctaacatc tctattccaa actgtggcgg ttacctggat accttggaag 1450

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gttgtctaca gattatgcca attcttaccg gggattttct gcttcctaca 1750

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gacaggatga gagttattat aagcaaatcc tacctagagg cttttaactc 1850

taatgggaat aacttgcaac taaaagaccc aacttgcaga ccaaaattat 1900

caaatgttgt ggaattttct gtccctctta atggatgtgg tacaatcaga 1950

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ccctaagtga gacatgtttc tccaggatgc caaaggaaat gctacctcgt 2850

ggctacacat attatgaata aatgaggaag ggcctgaaag tgacacacag 2900

gcctgcatgt aaaaaaa 2917

<210> 190
<211> 607
<212> PRT
<213> Homo Sapien

<400> 190

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				20				25						30	
Ser	Cys	Thr	Val	Ser	Leu	Gly	Gly	Ala	Asn	Met	Ala	Glu	Thr	His	
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Lys	Ala	Met	Ile	Leu	Gln	Leu	Asn	Pro	Ser	Glu	Asn	Cys	Thr	Trp	
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Thr	Ile	Glu	Arg	Pro	Glu	Asn	Lys	Ser	Ile	Arg	Ile	Ile	Phe	Ser	
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Tyr	Val	Gln	Leu	Asp	Pro	Asp	Gly	Ser	Cys	Glu	Ser	Glu	Asn	Ile	
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Lys	Val	Phe	Asp	Gly	Thr	Ser	Ser	Asn	Gly	Pro	Leu	Leu	Gly	Gln	
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Val	Cys	Ser	Lys	Asn	Asp	Tyr	Val	Pro	Val	Phe	Glu	Ser	Ser	Ser	
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Ser	Thr	Leu	Thr	Phe	Gln	Ile	Val	Thr	Asp	Ser	Ala	Arg	Ile	Gln	
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Arg	Thr	Val	Phe	Val	Phe	Tyr	Tyr	Phe	Phe	Ser	Pro	Asn	Ile	Ser	
				140				145						150	
Ile	Pro	Asn	Cys	Gly	Gly	Tyr	Leu	Asp	Thr	Leu	Glu	Gly	Ser	Phe	
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Thr	Ser	Pro	Asn	Tyr	Pro	Lys	Pro	His	Pro	Glu	Leu	Ala	Tyr	Cys	
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Val	Trp	His	Ile	Gln	Val	Glu	Lys	Asp	Tyr	Lys	Ile	Lys	Leu	Asn	

185 190 195

Phe Lys Glu Ile Phe Leu Glu Ile Asp Lys Gln Cys Lys Phe Asp
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Phe Leu Ala Ile Tyr Asp Gly Pro Ser Thr Asn Ser Gly Leu Ile
215 220 225

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230 235 240

Asn Ser Leu Thr Val Val Leu Ser Thr Asp Tyr Ala Asn Ser Tyr
245 250 255

Arg Gly Phe Ser Ala Ser Tyr Thr Ser Ile Tyr Ala Glu Asn Ile
260 265 270

Asn Thr Thr Ser Leu Thr Cys Ser Ser Asp Arg Met Arg Val Ile
275 280 285

Ile Ser Lys Ser Tyr Leu Glu Ala Phe Asn Ser Asn Gly Asn Asn
290 295 300

Leu Gln Leu Lys Asp Pro Thr Cys Arg Pro Lys Leu Ser Asn Val
305 310 315

Val Glu Phe Ser Val Pro Leu Asn Gly Cys Gly Thr Ile Arg Lys
320 325 330

Val Glu Asp Gln Ser Ile Thr Tyr Thr Asn Ile Ile Thr Phe Ser
335 340 345

Ala Ser Ser Thr Ser Glu Val Ile Thr Arg Gln Lys Gln Leu Gln
350 355 360

Ile Ile Val Lys Cys Glu Met Gly His Asn Ser Thr Val Glu Ile
365 370 375

Ile Tyr Ile Thr Glu Asp Asp Val Ile Gln Ser Gln Asn Ala Leu
380 385 390

Gly Lys Tyr Asn Thr Ser Met Ala Leu Phe Glu Ser Asn Ser Phe
395 400 405

Glu Lys Thr Ile Leu Glu Ser Pro Tyr Tyr Val Asp Leu Asn Gln
410 415 420

Thr Leu Phe Val Gln Val Ser Leu His Thr Ser Asp Pro Asn Leu
425 430 435

Val Val Phe Leu Asp Thr Cys Arg Ala Ser Pro Thr Ser Asp Phe
440 445 450

Ala Ser Pro Thr Tyr Asp Leu Ile Lys Ser Gly Cys Ser Arg Asp
455 460 465

Glu Thr Cys Lys Val Tyr Pro Leu Phe Gly His Tyr Gly Arg Phe
470 475 480

Gln Phe Asn Ala Phe Lys Phe Leu Arg Ser Met Ser Ser Val Tyr
485 490 495

Leu Gln Cys Lys Val Leu Ile Cys Asp Ser Ser Asp His Gln Ser

500 505 510

Arg Cys Asn Gln Gly Cys Val Ser Arg Ser Lys Arg Asp Ile Ser
515 520 525

Ser Tyr Lys Trp Lys Thr Asp Ser Ile Ile Gly Pro Ile Arg Leu
530 535 540

Lys Arg Asp Arg Ser Ala Ser Gly Asn Ser Gly Phe Gln His Glu
545 550 555

Thr His Ala Glu Glu Thr Pro Asn Gln Pro Phe Asn Ser Val His
560 565 570

Leu Phe Ser Phe Met Val Leu Ala Leu Asn Val Val Thr Val Ala
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Thr Ile Thr Val Arg His Phe Val Asn Gln Arg Ala Asp Tyr Lys
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Tyr Gln Lys Leu Gln Asn Tyr
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<210> 191
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 191
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<210> 192
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 192
tttgatgacg attcgaaggt gg 22

<210> 193
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 193
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<210> 194
<211> 2362
<212> DNA
<213> Homo Sapien

<400> 194
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cacagcgcca cgcgcttcga ccccacctgg gagtccctgg acgcccgcca 200
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tcctagtttc aaatatgaag attttggacc actatttaca gcaaaatttt 400
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<210> 195
<211> 467
<212> PRT
<213> Homo Sapien

<400> 195

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Ala Thr Arg Phe Asp Pro Thr Trp Glu Ser Leu Asp Ala Arg Gln
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Leu Pro Ala Trp Phe Asp Gln Ala Lys Phe Gly Ile Phe Ile His
             50                  55                  60

Trp Gly Val Phe Ser Val Pro Ser Phe Gly Ser Glu Trp Phe Trp
             65                  70                  75

Trp Tyr Trp Gln Lys Glu Lys Ile Pro Lys Tyr Val Glu Phe Met
             80                  85                  90

Lys Asp Asn Tyr Pro Pro Ser Phe Lys Tyr Glu Asp Phe Gly Pro
             95                 100                 105

Leu Phe Thr Ala Lys Phe Phe Asn Ala Asn Gln Trp Ala Asp Ile
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Phe Gln Ala Ser Gly Ala Lys Tyr Ile Val Leu Thr Ser Lys His
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His Glu Gly Phe Thr Leu Trp Gly Ser Glu Tyr Ser Trp Asn Trp
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Asn Ala Ile Asp Glu Gly Pro Lys Arg Asp Ile Val Lys Glu Leu
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Glu Val Ala Ile Arg Asn Arg Thr Asp Leu Arg Phe Gly Leu Tyr
                170                 175                 180

Tyr Ser Leu Phe Glu Trp Phe His Pro Leu Phe Leu Glu Asp Glu
                185                 190                 195

Ser Ser Ser Phe His Lys Arg Gln Phe Pro Val Ser Lys Thr Leu
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Pro Glu Leu Tyr Glu Leu Val Asn Asn Tyr Gln Pro Glu Val Leu
                215                 220                 225

Trp Ser Asp Gly Asp Gly Gly Ala Pro Asp Gln Tyr Trp Asn Ser
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Thr Gly Phe Leu Ala Trp Leu Tyr Asn Glu Ser Pro Val Arg Gly
                245                 250                 255

Thr Val Val Thr Asn Asp Arg Trp Gly Ala Gly Ser Ile Cys Lys
                260                 265                 270

His Gly Gly Phe Tyr Thr Cys Ser Asp Arg Tyr Asn Pro Gly His
                275                 280                 285

Leu Leu Pro His Lys Trp Glu Asn Cys Met Thr Ile Asp Lys Leu
                290                 295                 300

Ser Trp Gly Tyr Arg Arg Glu Ala Gly Ile Ser Asp Tyr Leu Thr
                305                 310                 315

Ile Glu Glu Leu Val Lys Gln Leu Val Glu Thr Val Ser Cys Gly
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Gly Asn Leu Leu Met Asn Ile Gly Pro Thr Leu Asp Gly Thr Ile
                335                 340                 345

Ser Val Val Phe Glu Glu Arg Leu Arg Gln Val Gly Ser Trp Leu
                350                 355                 360

Lys Val Asn Gly Glu Ala Ile Tyr Glu Thr Tyr Thr Trp Arg Ser
                365                 370                 375

Gln Asn Asp Thr Val Thr Pro Asp Val Trp Tyr Thr Ser Lys Pro
                380                 385                 390

Lys Glu Lys Leu Val Tyr Ala Ile Phe Leu Lys Trp Pro Thr Ser
                395                 400                 405

Gly Gln Leu Phe Leu Gly His Pro Lys Ala Ile Leu Gly Ala Thr
                410                 415                 420

Glu Val Lys Leu Leu Gly His Gly Gln Pro Leu Asn Trp Ile Ser
                425                 430                 435

Leu Glu Gln Asn Gly Ile Met Val Glu Leu Pro Gln Leu Thr Ile
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His Gln Met Pro Cys Lys Trp Gly Trp Ala Leu Ala Leu Thr Asn
455 460 465

Val Ile

<210> 196
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 196
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<210> 197
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 197
ggattcatcc tcaaggaaga gcgg 24

<210> 198
<211> 24
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<223> Synthetic Oligonucleotide Probe

<400> 198
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<210> 199
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 199
ttccgtgccc agcttcggta gcgagtggtt ctggtggtat tggca 45

<210> 200
<211> 2372
<212> DNA
<213> Homo Sapien

<400> 200
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cctctcatat caccagtggc catctgaggt gtttccctgg ctctgaaggg 150

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ataaatttct atttttatct gagttacaga aatgattact aaggaagatt 1950

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tagctactat atgtcaagtg ctgtgcaagg tattacactc tgtaattgaa 2050

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taccaaagca cattttaaaa gtgccattaa caaatgtatc actagccctc 2300

ctttttccaa caagaaggga ctgagagatg cagaaatatt tgtgacaaaa 2350

aattaaagca tttagaaaac tt 2372

<210> 201
<211> 322
<212> PRT
<213> Homo Sapien

<400> 201

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Ser	Ile	Gln	Val	Ser	Cys	Arg	Ile	Met	Gly	Ile	Thr	Leu	Val	Ser
				35				40						45
Lys	Lys	Ala	Asn	Gln	Gln	Leu	Asn	Phe	Thr	Glu	Ala	Lys	Glu	Ala
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Cys	Arg	Leu	Leu	Gly	Leu	Ser	Leu	Ala	Gly	Lys	Asp	Gln	Val	Glu
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Thr	Ala	Leu	Lys	Ala	Ser	Phe	Glu	Thr	Cys	Ser	Tyr	Gly	Trp	Val
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Gly	Asp	Gly	Phe	Val	Val	Ile	Ser	Arg	Ile	Ser	Pro	Asn	Pro	Lys
				95				100						105
Cys	Gly	Lys	Asn	Gly	Val	Gly	Val	Leu	Ile	Trp	Lys	Val	Pro	Val
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Ser	Arg	Gln	Phe	Ala	Ala	Tyr	Cys	Tyr	Asn	Ser	Ser	Asp	Thr	Trp
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Thr	Asn	Ser	Cys	Ile	Pro	Glu	Ile	Ile	Thr	Thr	Lys	Asp	Pro	Ile
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Asp Ser Thr Tyr Ser Val Ala Ser Pro Tyr Ser Thr Ile Pro Ala
170 175 180

Pro Thr Thr Thr Pro Pro Ala Pro Ala Ser Thr Ser Ile Pro Arg
185 190 195

Arg Lys Lys Leu Ile Cys Val Thr Glu Val Phe Met Glu Thr Ser
200 205 210

Thr Met Ser Thr Glu Thr Glu Pro Phe Val Glu Asn Lys Ala Ala
215 220 225

Phe Lys Asn Glu Ala Ala Gly Phe Gly Gly Val Pro Thr Ala Leu
230 235 240

Leu Val Leu Ala Leu Leu Phe Phe Gly Ala Ala Ala Gly Leu Gly
245 250 255

Phe Cys Tyr Val Lys Arg Tyr Val Lys Ala Phe Pro Phe Thr Asn
260 265 270

Lys Asn Gln Gln Lys Glu Met Ile Glu Thr Lys Val Val Lys Glu
275 280 285

Glu Lys Ala Asn Asp Ser Asn Pro Asn Glu Glu Ser Lys Lys Thr
290 295 300

Asp Lys Asn Pro Glu Glu Ser Lys Ser Pro Ser Lys Thr Thr Val
305 310 315

Arg Cys Leu Glu Ala Glu Val
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<210> 202
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<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 202
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<210> 203
<211> 22
<212> DNA
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<220>
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<400> 203
gtcagtgaca gtacctactc gg 22

<210> 204
<211> 24
<212> DNA
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<220>
<223> Synthetic Oligonucleotide Probe

<400> 204
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<210> 205
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<212> DNA
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<210> 206
<211> 1620
<212> DNA
<213> Homo Sapien

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<222> 973, 977, 996, 1003
<223> unknown base

<400> 206
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ctccctaccc tgatcctgtt ccaaggtggc aaggaggcaa tgcggcggcc 700

acagattgac aagaaaggac gggctgtctc atggaccttc tctgaggaga 750

atgtgatccg agaatttaac ttaaatgagc tataccagcg ggccaagaaa 800

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caagcctgag gctgcagcct ttnattnatg ttttcccttt ggctgngact 1000

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tcaggcaccc tacaggaagg cctgccatgc tgtggccaac tgtttcactg 1100

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gcttgggtca gtgtgttaac tgcttatcag ctattcagac atctccatgg 1200

tttctccatg aaactctgtg gtttcatcat tccttcttag ttgacctgca 1250

cagcttggtt agacctagat ttaaccctaa ggtaagatgc tggggtatag 1300

aacgctaaga attttccccc aaggactctt gcttccttaa gcccttctgg 1350

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aacaaccccc tattttgtgg ggattgagaa ggggtgaata gaggcttgag 1500

actttccttt gtgtggtagg acttggagga gaaatcccct ggactttcac 1550

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aagattggga tttccttttg 1620

<210> 207
<211> 296
<212> PRT
<213> Homo Sapien

<400> 207

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  1               5                  10                  15

Arg Leu Ser Arg Trp Leu Ala Gln Pro Tyr Tyr Leu Leu Ser Ala
             20                  25                  30

Leu Leu Ser Ala Ala Phe Leu Leu Val Arg Lys Leu Pro Pro Leu
             35                  40                  45

Cys His Gly Leu Pro Thr Gln Arg Glu Asp Gly Asn Pro Cys Asp
             50                  55                  60

Phe Asp Trp Arg Glu Val Glu Ile Leu Met Phe Leu Ser Ala Ile
             65                  70                  75

Val Met Met Lys Asn Arg Arg Ser Ile Thr Val Glu Gln His Ile
             80                  85                  90

Gly Asn Ile Phe Met Phe Ser Lys Val Ala Asn Thr Ile Leu Phe
             95                 100                 105

Phe Arg Leu Asp Ile Arg Met Gly Leu Leu Tyr Ile Thr Leu Cys
            110                 115                 120

Ile Val Phe Leu Met Thr Cys Lys Pro Pro Leu Tyr Met Gly Pro
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125 130 135

Glu Tyr Ile Lys Tyr Phe Asn Asp Lys Thr Ile Asp Glu Glu Leu
140 145 150

Glu Arg Asp Lys Arg Val Thr Trp Ile Val Glu Phe Phe Ala Asn
155 160 165

Trp Ser Asn Asp Cys Gln Ser Phe Ala Pro Ile Tyr Ala Asp Leu
170 175 180

Ser Leu Lys Tyr Asn Cys Thr Gly Leu Asn Phe Gly Lys Val Asp
185 190 195

Val Gly Arg Tyr Thr Asp Val Ser Thr Arg Tyr Lys Val Ser Thr
200 205 210

Ser Pro Leu Thr Lys Gln Leu Pro Thr Leu Ile Leu Phe Gln Gly
215 220 225

Gly Lys Glu Ala Met Arg Arg Pro Gln Ile Asp Lys Lys Gly Arg
230 235 240

Ala Val Ser Trp Thr Phe Ser Glu Glu Asn Val Ile Arg Glu Phe
245 250 255

Asn Leu Asn Glu Leu Tyr Gln Arg Ala Lys Lys Leu Ser Lys Ala
260 265 270

Gly Asp Asn Ile Pro Glu Glu Gln Pro Val Ala Ser Thr Pro Thr
275 280 285

Thr Val Ser Asp Gly Glu Asn Lys Lys Asp Lys
290 295

<210> 208
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 208
gcttggatat tcgcatgggc ctac 24

<210> 209
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 209
tggagacaat atccctgagg 20

<210> 210
<211> 24
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 210
aacagttggc cacagcatgg cagg 24

<210> 211
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 211
ccattgatga ggaactagaa cgggacaaga gggtcacttg gattgtggag 50

<210> 212
<211> 1985
<212> DNA
<213> Homo Sapien

<400> 212
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acgtttgccc tggggcccca gcctggcccg ggtcaccctg gcatgaggag 100

atgggcctgt tgctcctggt cccattgctc ctgctgcccg gctcctacgg 150

actgcccttc tacaacggct tctactactc caacagcgcc aacgaccaga 200

acctaggcaa cggtcatggc aaagacctcc ttaatggagt gaagctggtg 250

gtggagacac ccgaggagac cctgttcacc taccaagggg ccagtgtgat 300

cctgccctgc cgctaccgct acgagccggc cctggtctcc ccgcggcgtg 350

tgcgtgtcaa atggtggaag ctgtcggaga acggggcccc agagaaggac 400

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ccccagagcc tggggtccga agctttggct tccccgaccc gcagagccgc 1150

ttgtacggtg tttactgcta ccgccagcac taggacctgg ggccctcccc 1200

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tgtgggttgg agccatttta actgttttta tacttctcaa tttaaatttt 1300

ctttaaacat ttttttacta ttttttgtaa agcaaacaga acccaatgcc 1350

tccctttgct cctggatgcc ccactccagg aatcatgctt gctcccctgg 1400

gccatttgcg gttttgtggg cttctggagg gttccccgcc atccaggctg 1450

gtctccctcc cttaaggagg ttggtgccca gagtgggcgg tggcctgtct 1500

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cagcctgggg gaagaagagg gcctcggggg cctccggagc tgggctttgg 1600

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caaagaatct gttttgttgt catttgtttc tcctgtttcc ctgtgtgggg 1800

aggggccctc aggtgtgtgt actttggaca ataaatggtg ctatgactgc 1850

cttccgccaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1900

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1950

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaa 1985

<210> 213
<211> 360
<212> PRT
<213> Homo Sapien

<400> 213

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Tyr	Gly	Leu	Pro	Phe	Tyr	Asn	Gly	Phe	Tyr	Tyr	Ser	Asn	Ser	Ala	
				20				25						30	
Asn	Asp	Gln	Asn	Leu	Gly	Asn	Gly	His	Gly	Lys	Asp	Leu	Leu	Asn	
				35				40						45	
Gly	Val	Lys	Leu	Val	Val	Glu	Thr	Pro	Glu	Glu	Thr	Leu	Phe	Thr	
				50				55						60	
Tyr	Gln	Gly	Ala	Ser	Val	Ile	Leu	Pro	Cys	Arg	Tyr	Arg	Tyr	Glu	
				65				70						75	
Pro	Ala	Leu	Val	Ser	Pro	Arg	Arg	Val	Arg	Val	Lys	Trp	Trp	Lys	
				80				85						90	

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Leu Ser Glu Asn Gly Ala Pro Glu Lys Asp Val Leu Val Ala Ile
 95                  100                 105

Gly Leu Arg His Arg Ser Phe Gly Asp Tyr Gln Gly Arg Val His
110                 115                 120

Leu Arg Gln Asp Lys Glu His Asp Val Ser Leu Glu Ile Gln Asp
125                 130                 135

Leu Arg Leu Glu Asp Tyr Gly Arg Tyr Arg Cys Glu Val Ile Asp
140                 145                 150

Gly Leu Glu Asp Glu Ser Gly Leu Val Glu Leu Glu Leu Arg Gly
155                 160                 165

Val Val Phe Pro Tyr Gln Ser Pro Asn Gly Arg Tyr Gln Phe Asn
170                 175                 180

Phe His Glu Gly Gln Gln Val Cys Ala Glu Gln Ala Ala Val Val
185                 190                 195

Ala Ser Phe Glu Gln Leu Phe Arg Ala Trp Glu Glu Gly Leu Asp
200                 205                 210

Trp Cys Asn Ala Gly Trp Leu Gln Asp Ala Thr Val Gln Tyr Pro
215                 220                 225

Ile Met Leu Pro Arg Gln Pro Cys Gly Gly Pro Gly Leu Ala Pro
230                 235                 240

Gly Val Arg Ser Tyr Gly Pro Arg His Arg Arg Leu His Arg Tyr
245                 250                 255

Asp Val Phe Cys Phe Ala Thr Ala Leu Lys Gly Arg Val Tyr Tyr
260                 265                 270

Leu Glu His Pro Glu Lys Leu Thr Leu Thr Glu Ala Arg Glu Ala
275                 280                 285

Cys Gln Glu Asp Asp Ala Thr Ile Ala Lys Val Gly Gln Leu Phe
290                 295                 300

Ala Ala Trp Lys Phe His Gly Leu Asp Arg Cys Asp Ala Gly Trp
305                 310                 315

Leu Ala Asp Gly Ser Val Arg Tyr Pro Val Val His Pro His Pro
320                 325                 330

Asn Cys Gly Pro Pro Glu Pro Gly Val Arg Ser Phe Gly Phe Pro
335                 340                 345

Asp Pro Gln Ser Arg Leu Tyr Gly Val Tyr Cys Tyr Arg Gln His
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<210> 214
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 214

tgcttcgcta ctgccctc 18

<210> 215
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 215
ttcccttgtg ggttggag 18

<210> 216
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 216
agggctggaa gccagttc 18

<210> 217
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 217
agccagtgag gaaatgcg 18

<210> 218
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 218
tgtccaaagt acacacacct gagg 24

<210> 219
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 219
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<210> 220
<211> 1503
<212> DNA
<213> Homo Sapien

<400> 220

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cctgagcgac gctccccatg atgacgccca cgggaacttc cagtacgacc 200

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ccagaggaaa gccaggcccg tctggggcgg atcgtggacc gcatggaccg 300

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gacacgtacg acacggaccg cgacgggcgt gtgggttggg aggagctgcg 450

caacgccacc tatggccact acgcgcccgg tgaagaattt catgacgtgg 500

aggatgcaga gacctacaaa aagatgctgg ctcgggacga gcggcgtttc 550

cgggtggccg accaggatgg ggactcgatg gccactcgag aggagctgac 600

agccttcctg caccccgagg agttccctca catgcgggac atcgtgattg 650

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gaggagtaca tcgcggatct gtactcagcc gagcctgggg aggaggagcc 750

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acaaggatgg gcacctggat gggagtgagg tgggccactg ggtgctgccc 850

cctgcccagg accagccccc ggtggaagcc aaccacctgc tgcacgagag 900

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cggcaccacg atgagctgtg agcaccgcgc acctgccaca gcctcagagg 1050

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actgaaactc ccctggcccc agccctctcc tgcctggcct ggcctgggac 1400

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aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1500

aaa 1503

<210> 221

<211> 328
<212> PRT
<213> Homo Sapien

<400> 221

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Met Met Trp Arg Pro Ser Val Leu Leu Leu Leu Leu Leu Leu Arg
  1               5                  10                  15

His Gly Ala Gln Gly Lys Pro Ser Pro Asp Ala Gly Pro His Gly
             20                  25                  30

Gln Gly Arg Val His Gln Ala Ala Pro Leu Ser Asp Ala Pro His
             35                  40                  45

Asp Asp Ala His Gly Asn Phe Gln Tyr Asp His Glu Ala Phe Leu
             50                  55                  60

Gly Arg Glu Val Ala Lys Glu Phe Asp Gln Leu Thr Pro Glu Glu
             65                  70                  75

Ser Gln Ala Arg Leu Gly Arg Ile Val Asp Arg Met Asp Arg Ala
             80                  85                  90

Gly Asp Gly Asp Gly Trp Val Ser Leu Ala Glu Leu Arg Ala Trp
             95                 100                 105

Ile Ala His Thr Gln Gln Arg His Ile Arg Asp Ser Val Ser Ala
            110                 115                 120

Ala Trp Asp Thr Tyr Asp Thr Asp Arg Asp Gly Arg Val Gly Trp
            125                 130                 135

Glu Glu Leu Arg Asn Ala Thr Tyr Gly His Tyr Ala Pro Gly Glu
            140                 145                 150

Glu Phe His Asp Val Glu Asp Ala Glu Thr Tyr Lys Lys Met Leu
            155                 160                 165

Ala Arg Asp Glu Arg Arg Phe Arg Val Ala Asp Gln Asp Gly Asp
            170                 175                 180

Ser Met Ala Thr Arg Glu Glu Leu Thr Ala Phe Leu His Pro Glu
            185                 190                 195

Glu Phe Pro His Met Arg Asp Ile Val Ile Ala Glu Thr Leu Glu
            200                 205                 210

Asp Leu Asp Arg Asn Lys Asp Gly Tyr Val Gln Val Glu Glu Tyr
            215                 220                 225

Ile Ala Asp Leu Tyr Ser Ala Glu Pro Gly Glu Glu Glu Pro Ala
            230                 235                 240

Trp Val Gln Thr Glu Arg Gln Gln Phe Arg Asp Phe Arg Asp Leu
            245                 250                 255

Asn Lys Asp Gly His Leu Asp Gly Ser Glu Val Gly His Trp Val
            260                 265                 270

Leu Pro Pro Ala Gln Asp Gln Pro Leu Val Glu Ala Asn His Leu
            275                 280                 285

Leu His Glu Ser Asp Thr Asp Lys Asp Gly Arg Leu Ser Lys Ala
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290 295 300

Glu Ile Leu Gly Asn Trp Asn Met Phe Val Gly Ser Gln Ala Thr
305 310 315

Asn Tyr Gly Glu Asp Leu Thr Arg His His Asp Glu Leu
320 325

<210> 222
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 222
cgcaggccct catggccagg 20

<210> 223
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 223
gaaatcctgg gtaattgg 18

<210> 224
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 224
gtgcgcggtg ctcacagctc atc 23

<210> 225
<211> 44
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 225
ccccccctgag cgacgctccc ccatgatgac gcccacggga actt 44

<210> 226
<211> 2403
<212> DNA
<213> Homo Sapien

<400> 226
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gcggagcccc gggcggcggg cgcgggtgcg agggatccct gacgcctctg 100

tccctgtttc tttgtcgctc ccagcctgtc tgtcgtcgtt ttggcgcccc 150

cgcctccccg cggtgcgggg ttgcacaccg atcctgggct tcgctcgatt 200

tgccgccgag gcgcctccca gacctagagg ggcgctggcc tggagcagcg 250

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gcggggctct gaggaggtga cgcgcggggc ctcccgcacc ctggccttgc 350

ccgcattctc cctctctccc aggtgtgagc agcctatcag tcaccatgtc 400

cgcagcctgg atcccggctc tcggcctcgg tgtgtgtctg ctgctgctgc 450

cggggcccgc gggcagcgag ggagccgctc ccattgctat cacatgtttt 500

accagaggct tggacatcag gaaagagaaa gcagatgtcc tctgcccagg 550

gggctgccct cttgaggaat tctctgtgta tgggaacata gtatatgctt 600

ctgtatcgag catatgtggg gctgctgtcc acaggggagt aatcagcaac 650

tcagggggac ctgtacgagt ctatagccta cctggtcgag aaaactattc 700

ctcagtagat gccaatggca tccagtctca aatgctttct agatggtctg 750

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caagcagtgt ccacagcaca tccaccaaca ggtaaacgac taaagaaaac 850

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tgattgatgg aagctttaat attgggcagc gccgatttaa tttacagaag 950

aattttgttg gaaaagtggc tctaatgttg ggaattggaa cagaaggacc 1000

acatgtgggc cttgttcaag ccagtgaaca tcccaaaata gaattttact 1050

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ggtttcagag ggggtaattc caatacagga aaagccttga agcatactgc 1150

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caagcctatc cctgaagaac tggggatggt tcaggatgtc acatttgttg 1350

acaaggctgt ctgtcggaat aatggcttct tctcttacca catgcccaac 1400

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tcatgaacaa atgatgtgca gcaagacctg ttataactca gtgaacattg 1500

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gcagctgctg cacatgatgc aggaatcact atcttctctg ttggtgtggc 1900

ttgggcacct ctggatgacc tgaaagatat ggcttctaaa ccgaaggagt 1950

ctcacgcttt cttcacaaga gagttcacag gattagaacc aattgtttct 2000

gatgtcatca gaggcatttg tagagatttc ttagaatccc agcaataatg 2050

gtaacatttt gacaactgaa agaaaaagta caaggggatc cagtgtgtaa 2100

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aaa 2403

<210> 227
<211> 550
<212> PRT
<213> Homo Sapien

<400> 227

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Met Ser Ala Ala Trp Ile Pro Ala Leu Gly Leu Gly Val Cys Leu
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Leu Leu Leu Pro Gly Pro Ala Gly Ser Glu Gly Ala Ala Pro Ile
             20                  25                  30

Ala Ile Thr Cys Phe Thr Arg Gly Leu Asp Ile Arg Lys Glu Lys
             35                  40                  45

Ala Asp Val Leu Cys Pro Gly Gly Cys Pro Leu Glu Glu Phe Ser
             50                  55                  60

Val Tyr Gly Asn Ile Val Tyr Ala Ser Val Ser Ser Ile Cys Gly
             65                  70                  75

Ala Ala Val His Arg Gly Val Ile Ser Asn Ser Gly Gly Pro Val
             80                  85                  90

Arg Val Tyr Ser Leu Pro Gly Arg Glu Asn Tyr Ser Ser Val Asp
             95                 100                 105

Ala Asn Gly Ile Gln Ser Gln Met Leu Ser Arg Trp Ser Ala Ser
            110                 115                 120

Phe Thr Val Thr Lys Gly Lys Ser Ser Thr Gln Glu Ala Thr Gly
            125                 130                 135
```

```
Gln Ala Val Ser Thr Ala His Pro Pro Thr Gly Lys Arg Leu Lys
                140                 145                 150

Lys Thr Pro Glu Lys Lys Thr Gly Asn Lys Asp Cys Lys Ala Asp
                155                 160                 165

Ile Ala Phe Leu Ile Asp Gly Ser Phe Asn Ile Gly Gln Arg Arg
                170                 175                 180

Phe Asn Leu Gln Lys Asn Phe Val Gly Lys Val Ala Leu Met Leu
                185                 190                 195

Gly Ile Gly Thr Glu Gly Pro His Val Gly Leu Val Gln Ala Ser
                200                 205                 210

Glu His Pro Lys Ile Glu Phe Tyr Leu Lys Asn Phe Thr Ser Ala
                215                 220                 225

Lys Asp Val Leu Phe Ala Ile Lys Glu Val Gly Phe Arg Gly Gly
                230                 235                 240

Asn Ser Asn Thr Gly Lys Ala Leu Lys His Thr Ala Gln Lys Phe
                245                 250                 255

Phe Thr Val Asp Ala Gly Val Arg Lys Gly Ile Pro Lys Val Val
                260                 265                 270

Val Val Phe Ile Asp Gly Trp Pro Ser Asp Asp Ile Glu Glu Ala
                275                 280                 285

Gly Ile Val Ala Arg Glu Phe Gly Val Asn Val Phe Ile Val Ser
                290                 295                 300

Val Ala Lys Pro Ile Pro Glu Glu Leu Gly Met Val Gln Asp Val
                305                 310                 315

Thr Phe Val Asp Lys Ala Val Cys Arg Asn Asn Gly Phe Phe Ser
                320                 325                 330

Tyr His Met Pro Asn Trp Phe Gly Thr Thr Lys Tyr Val Lys Pro
                335                 340                 345

Leu Val Gln Lys Leu Cys Thr His Glu Gln Met Met Cys Ser Lys
                350                 355                 360

Thr Cys Tyr Asn Ser Val Asn Ile Ala Phe Leu Ile Asp Gly Ser
                365                 370                 375

Ser Ser Val Gly Asp Ser Asn Phe Arg Leu Met Leu Glu Phe Val
                380                 385                 390

Ser Asn Ile Ala Lys Thr Phe Glu Ile Ser Asp Ile Gly Ala Lys
                395                 400                 405

Ile Ala Ala Val Gln Phe Thr Tyr Asp Gln Arg Thr Glu Phe Ser
                410                 415                 420

Phe Thr Asp Tyr Ser Thr Lys Glu Asn Val Leu Ala Val Ile Arg
                425                 430                 435

Asn Ile Arg Tyr Met Ser Gly Gly Thr Ala Thr Gly Asp Ala Ile
                440                 445                 450
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Ser Phe Thr Val Arg Asn Val Phe Gly Pro Ile Arg Glu Ser Pro
455 460 465

Asn Lys Asn Phe Leu Val Ile Val Thr Asp Gly Gln Ser Tyr Asp
470 475 480

Asp Val Gln Gly Pro Ala Ala Ala Ala His Asp Ala Gly Ile Thr
485 490 495

Ile Phe Ser Val Gly Val Ala Trp Ala Pro Leu Asp Asp Leu Lys
500 505 510

Asp Met Ala Ser Lys Pro Lys Glu Ser His Ala Phe Phe Thr Arg
515 520 525

Glu Phe Thr Gly Leu Glu Pro Ile Val Ser Asp Val Ile Arg Gly
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Ile Cys Arg Asp Phe Leu Glu Ser Gln Gln
545 550

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<220>
<223> Synthetic Oligonucleotide Probe

<400> 228
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<210> 229
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<210> 230
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gagatagcaa tttccgcc 18

<210> 232
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<220>
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<400> 232
ttcctcaaga gggcagcc 18

<210> 233
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<220>
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<400> 233
cttggcacca atgtccgaga tttc 24

<210> 234
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<400> 234
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<210> 235
<211> 2586
<212> DNA
<213> Homo Sapien

<400> 235
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cacccgcagc ccggcggcct cccggcggga gcgagcagat ccagtccggc 100

ccgcagcgca actcggtcca gtcggggcgg cggctgcggg cgcagagcgg 150

agatgcagcg gcttggggcc accctgctgt gcctgctgct ggcggcggcg 200

gtccccacgg cccccgcgcc cgctccgacg gcgacctcgg ctccagtcaa 250

gcccggcccg gctctcagct acccgcagga ggaggccacc ctcaatgaga 300

tgttccgcga ggttgaggaa ctgatggagg acacgcagca caaattgcgc 350

agcgcggtgg aagagatgga ggcagaagaa gctgctgcta aagcatcatc 400

agaagtgaac ctggcaaact tacctcccag ctatcacaat gagaccaaca 450

cagacacgaa ggttggaaat aataccatcc atgtgcaccg agaaattcac 500

aagataacca acaaccagac tggacaaatg gtcttttcag agacagttat 550

cacatctgtg ggagacgaag aaggcagaag gagccacgag tgcatcatcg 600

acgaggactg tgggcccagc atgtactgcc agtttgccag cttccagtac 650

acctgccagc catgccgggg ccagaggatg ctctgcaccc gggacagtga 700

gtgctgtgga gaccagctgt gtgtctgggg tcactgcacc aaaatggcca 750

ccaggggcag caatgggacc atctgtgaca accagaggga ctgccagccg 800

gggctgtgct gtgccttcca gagaggcctg ctgttccctg tgtgcacacc 850

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catcttcttc ccagtaagtt tcccctctgg cttgacagca tgaggtgttg 1350

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tccagattat tggctgcttt gcctctacca gttggcagac agccgtttgt 1500

tctacatggc tttgataatt gtttgagggg aggagatgga aacaatgtgg 1550

agtctccctc tgattggttt tggggaaatg tggagaagag tgccctgctt 1600

tgcaaacatc aacctggcaa aaatgcaaca aatgaatttt ccacgcagtt 1650

ctttccatgg gcataggtaa gctgtgcctt cagctgttgc agatgaaatg 1700

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tttaaattat gtataaacat aagttgcatt tagaaatcaa gcataaatca 2550

cttcaactgc aaaaaaaaaa aaaaaaaaaa aaaaaa 2586

<210> 236
<211> 350
<212> PRT
<213> Homo Sapien

<400> 236

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Ala	Val	Pro	Thr	Ala	Pro	Ala	Pro	Ala	Pro	Thr	Ala	Thr	Ser	Ala	
				20					25						30
Pro	Val	Lys	Pro	Gly	Pro	Ala	Leu	Ser	Tyr	Pro	Gln	Glu	Glu	Ala	
				35					40						45
Thr	Leu	Asn	Glu	Met	Phe	Arg	Glu	Val	Glu	Glu	Leu	Met	Glu	Asp	
				50					55						60
Thr	Gln	His	Lys	Leu	Arg	Ser	Ala	Val	Glu	Glu	Met	Glu	Ala	Glu	
				65					70						75
Glu	Ala	Ala	Ala	Lys	Ala	Ser	Ser	Glu	Val	Asn	Leu	Ala	Asn	Leu	
				80					85						90
Pro	Pro	Ser	Tyr	His	Asn	Glu	Thr	Asn	Thr	Asp	Thr	Lys	Val	Gly	
				95					100						105
Asn	Asn	Thr	Ile	His	Val	His	Arg	Glu	Ile	His	Lys	Ile	Thr	Asn	
				110					115						120
Asn	Gln	Thr	Gly	Gln	Met	Val	Phe	Ser	Glu	Thr	Val	Ile	Thr	Ser	
				125					130						135
Val	Gly	Asp	Glu	Glu	Gly	Arg	Arg	Ser	His	Glu	Cys	Ile	Ile	Asp	
				140					145						150
Glu	Asp	Cys	Gly	Pro	Ser	Met	Tyr	Cys	Gln	Phe	Ala	Ser	Phe	Gln	
				155					160						165
Tyr	Thr	Cys	Gln	Pro	Cys	Arg	Gly	Gln	Arg	Met	Leu	Cys	Thr	Arg	
				170					175						180
Asp	Ser	Glu	Cys	Cys	Gly	Asp	Gln	Leu	Cys	Val	Trp	Gly	His	Cys	
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Thr Lys Met Ala Thr Arg Gly Ser Asn Gly Thr Ile Cys Asp Asn
200 205 210

Gln Arg Asp Cys Gln Pro Gly Leu Cys Cys Ala Phe Gln Arg Gly
215 220 225

Leu Leu Phe Pro Val Cys Thr Pro Leu Pro Val Glu Gly Glu Leu
230 235 240

Cys His Asp Pro Ala Ser Arg Leu Leu Asp Leu Ile Thr Trp Glu
245 250 255

Leu Glu Pro Asp Gly Ala Leu Asp Arg Cys Pro Cys Ala Ser Gly
260 265 270

Leu Leu Cys Gln Pro His Ser His Ser Leu Val Tyr Val Cys Lys
275 280 285

Pro Thr Phe Val Gly Ser Arg Asp Gln Asp Gly Glu Ile Leu Leu
290 295 300

Pro Arg Glu Val Pro Asp Glu Tyr Glu Val Gly Ser Phe Met Glu
305 310 315

Glu Val Arg Gln Glu Leu Glu Asp Leu Glu Arg Ser Leu Thr Glu
320 325 330

Glu Met Ala Leu Gly Glu Pro Ala Ala Ala Ala Ala Ala Leu Leu
335 340 345

Gly Gly Glu Glu Ile
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<210> 237
<211> 17
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<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 237
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<210> 238
<211> 49
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 238
ggaggactgt gccaccatga gagactcttc aaacccaagg caaaattgg 49

<210> 239
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 239
gcagagcgga gatgcagcgg cttg 24

<210> 240
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 240
ttggcagctt catggagg 18

<210> 241
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 241
cctgggcaaa aatgcaac 18

<210> 242
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 242
ctccagctcc tggcgcacct cctc 24

<210> 243
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 243
ggctctcagc taccgcgcag gagcgaggcc accctcaatg agatg 45

<210> 244
<211> 3679
<212> DNA
<213> Homo Sapien

<400> 244
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tctctctggg ctcagaagga ctctgaagat aacaataatt tcagcccatc 100

cactctcctt ccctcccaaa cacacatgtg catgtacaca cacacataca 150

cacacataca ccttcctctc cttcactgaa gactcacagt cactcactct 200

gtgagcaggt catagaaaag gacactaaag ccttaaggac aggcctggcc 250

attacctctg cagctccttt ggcttgttga gtcaaaaaac atgggagggg 300
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<210> 245
<211> 713
<212> PRT
<213> Homo Sapien

<400> 245

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Ala Thr Ala Thr Val Pro Val Val Pro Trp His Val Pro Cys Pro
             20                  25                  30

Pro Gln Cys Ala Cys Gln Ile Arg Pro Trp Tyr Thr Pro Arg Ser
             35                  40                  45

Ser Tyr Arg Glu Ala Thr Thr Val Asp Cys Asn Asp Leu Phe Leu
             50                  55                  60

Thr Ala Val Pro Pro Ala Leu Pro Ala Gly Thr Gln Thr Leu Leu
             65                  70                  75

Leu Gln Ser Asn Ser Ile Val Arg Val Asp Gln Ser Glu Leu Gly
             80                  85                  90

Tyr Leu Ala Asn Leu Thr Glu Leu Asp Leu Ser Gln Asn Ser Phe
             95                 100                 105

Ser Asp Ala Arg Asp Cys Asp Phe His Ala Leu Pro Gln Leu Leu
            110                 115                 120

Ser Leu His Leu Glu Glu Asn Gln Leu Thr Arg Leu Glu Asp His
            125                 130                 135

Ser Phe Ala Gly Leu Ala Ser Leu Gln Glu Leu Tyr Leu Asn His
            140                 145                 150

Asn Gln Leu Tyr Arg Ile Ala Pro Arg Ala Phe Ser Gly Leu Ser
            155                 160                 165

Asn Leu Leu Arg Leu His Leu Asn Ser Asn Leu Leu Arg Ala Ile
            170                 175                 180

Asp Ser Arg Trp Phe Glu Met Leu Pro Asn Leu Glu Ile Leu Met
            185                 190                 195

Ile Gly Gly Asn Lys Val Asp Ala Ile Leu Asp Met Asn Phe Arg
            200                 205                 210

Pro Leu Ala Asn Leu Arg Ser Leu Val Leu Ala Gly Met Asn Leu
            215                 220                 225
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Arg Glu Ile Ser Asp Tyr Ala Leu Glu Gly Leu Gln Ser Leu Glu
                230                 235                 240

Ser Leu Ser Phe Tyr Asp Asn Gln Leu Ala Arg Val Pro Arg Arg
                245                 250                 255

Ala Leu Glu Gln Val Pro Gly Leu Lys Phe Leu Asp Leu Asn Lys
                260                 265                 270

Asn Pro Leu Gln Arg Val Gly Pro Gly Asp Phe Ala Asn Met Leu
                275                 280                 285

His Leu Lys Glu Leu Gly Leu Asn Asn Met Glu Glu Leu Val Ser
                290                 295                 300

Ile Asp Lys Phe Ala Leu Val Asn Leu Pro Glu Leu Thr Lys Leu
                305                 310                 315

Asp Ile Thr Asn Asn Pro Arg Leu Ser Phe Ile His Pro Arg Ala
                320                 325                 330

Phe His His Leu Pro Gln Met Glu Thr Leu Met Leu Asn Asn Asn
                335                 340                 345

Ala Leu Ser Ala Leu His Gln Gln Thr Val Glu Ser Leu Pro Asn
                350                 355                 360

Leu Gln Glu Val Gly Leu His Gly Asn Pro Ile Arg Cys Asp Cys
                365                 370                 375

Val Ile Arg Trp Ala Asn Ala Thr Gly Thr Arg Val Arg Phe Ile
                380                 385                 390

Glu Pro Gln Ser Thr Leu Cys Ala Glu Pro Pro Asp Leu Gln Arg
                395                 400                 405

Leu Pro Val Arg Glu Val Pro Phe Arg Glu Met Thr Asp His Cys
                410                 415                 420

Leu Pro Leu Ile Ser Pro Arg Ser Phe Pro Pro Ser Leu Gln Val
                425                 430                 435

Ala Ser Gly Glu Ser Met Val Leu His Cys Arg Ala Leu Ala Glu
                440                 445                 450

Pro Glu Pro Glu Ile Tyr Trp Val Thr Pro Ala Gly Leu Arg Leu
                455                 460                 465

Thr Pro Ala His Ala Gly Arg Arg Tyr Arg Val Tyr Pro Glu Gly
                470                 475                 480

Thr Leu Glu Leu Arg Arg Val Thr Ala Glu Glu Ala Gly Leu Tyr
                485                 490                 495

Thr Cys Val Ala Gln Asn Leu Val Gly Ala Asp Thr Lys Thr Val
                500                 505                 510

Ser Val Val Val Gly Arg Ala Leu Leu Gln Pro Gly Arg Asp Glu
                515                 520                 525

Gly Gln Gly Leu Glu Leu Arg Val Gln Glu Thr His Pro Tyr His
                530                 535                 540
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Ile Leu Leu Ser Trp Val Thr Pro Pro Asn Thr Val Ser Thr Asn
545 550 555

Leu Thr Trp Ser Ser Ala Ser Ser Leu Arg Gly Gln Gly Ala Thr
560 565 570

Ala Leu Ala Arg Leu Pro Arg Gly Thr His Ser Tyr Asn Ile Thr
575 580 585

Arg Leu Leu Gln Ala Thr Glu Tyr Trp Ala Cys Leu Gln Val Ala
590 595 600

Phe Ala Asp Ala His Thr Gln Leu Ala Cys Val Trp Ala Arg Thr
605 610 615

Lys Glu Ala Thr Ser Cys His Arg Ala Leu Gly Asp Arg Pro Gly
620 625 630

Leu Ile Ala Ile Leu Ala Leu Ala Val Leu Leu Leu Ala Ala Gly
635 640 645

Leu Ala Ala His Leu Gly Thr Gly Gln Pro Arg Lys Gly Val Gly
650 655 660

Gly Arg Arg Pro Leu Pro Pro Ala Trp Ala Phe Trp Gly Trp Ser
665 670 675

Ala Pro Ser Val Arg Val Val Ser Ala Pro Leu Val Leu Pro Trp
680 685 690

Asn Pro Gly Arg Lys Leu Pro Arg Ser Ser Glu Gly Glu Thr Leu
695 700 705

Leu Pro Pro Leu Ser Gln Asn Ser
710

<210> 246
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 246
aacaaggtaa gatgccatcc tg 22

<210> 247
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 247
aaacttgtcg atggagacca gctc 24

<210> 248
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
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<400> 248
aggggctgca aagcctggag agcctctcct tctatgacaa ccagc 45

<210> 249
<211> 3401
<212> DNA
<213> Homo Sapien

<400> 249
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catcaagttc gacgtggact gcaccgtgga cattgagagc ctgacgggct 200

accgcaccta ccgctgtgcc cacccctgg ccacactctt caagatcctg 250

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ccctgacact gtgtttgacc tggtggagct ggaggtcctc aagctggagc 650

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<211> 546
<212> PRT
<213> Homo Sapien

<400> 250

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				20				25						30	
Cys	Thr	Val	Asp	Ile	Glu	Ser	Leu	Thr	Gly	Tyr	Arg	Thr	Tyr	Arg	
				35				40						45	
Cys	Ala	His	Pro	Leu	Ala	Thr	Leu	Phe	Lys	Ile	Leu	Ala	Ser	Phe	
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Tyr	Ile	Ser	Leu	Val	Ile	Phe	Tyr	Gly	Leu	Ile	Cys	Met	Tyr	Thr	
				65				70						75	
Leu	Trp	Trp	Met	Leu	Arg	Arg	Ser	Leu	Lys	Lys	Tyr	Ser	Phe	Glu	
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Ser	Ile	Arg	Glu	Glu	Ser	Ser	Tyr	Ser	Asp	Ile	Pro	Asp	Val	Lys	
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Asn	Asp	Phe	Ala	Phe	Met	Leu	His	Leu	Ile	Asp	Gln	Tyr	Asp	Pro	
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Leu	Tyr	Ser	Lys	Arg	Phe	Ala	Val	Phe	Leu	Ser	Glu	Val	Ser	Glu	
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Asn	Lys	Leu	Arg	Gln	Leu	Asn	Leu	Asn	Asn	Glu	Trp	Thr	Leu	Asp	
				140				145						150	
Lys	Leu	Arg	Gln	Arg	Leu	Thr	Lys	Asn	Ala	Gln	Asp	Lys	Leu	Glu	
				155				160						165	

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Leu His Leu Phe Met Leu Ser Gly Ile Pro Asp Thr Val Phe Asp
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Leu Val Glu Leu Glu Val Leu Lys Leu Glu Leu Ile Pro Asp Val
                185                 190                 195

Thr Ile Pro Pro Ser Ile Ala Gln Leu Thr Gly Leu Lys Glu Leu
                200                 205                 210

Trp Leu Tyr His Thr Ala Ala Lys Ile Glu Ala Pro Ala Leu Ala
                215                 220                 225

Phe Leu Arg Glu Asn Leu Arg Ala Leu His Ile Lys Phe Thr Asp
                230                 235                 240

Ile Lys Glu Ile Pro Leu Trp Ile Tyr Ser Leu Lys Thr Leu Glu
                245                 250                 255

Glu Leu His Leu Thr Gly Asn Leu Ser Ala Glu Asn Asn Arg Tyr
                260                 265                 270

Ile Val Ile Asp Gly Leu Arg Glu Leu Lys Arg Leu Lys Val Leu
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Arg Leu Lys Ser Asn Leu Ser Lys Leu Pro Gln Val Val Thr Asp
                290                 295                 300

Val Gly Val His Leu Gln Lys Leu Ser Ile Asn Asn Glu Gly Thr
                305                 310                 315

Lys Leu Ile Val Leu Asn Ser Leu Lys Lys Met Ala Asn Leu Thr
                320                 325                 330

Glu Leu Glu Leu Ile Arg Cys Asp Leu Glu Arg Ile Pro His Ser
                335                 340                 345

Ile Phe Ser Leu His Asn Leu Gln Glu Ile Asp Leu Lys Asp Asn
                350                 355                 360

Asn Leu Lys Thr Ile Glu Glu Ile Ile Ser Phe Gln His Leu His
                365                 370                 375

Arg Leu Thr Cys Leu Lys Leu Trp Tyr Asn His Ile Ala Tyr Ile
                380                 385                 390

Pro Ile Gln Ile Gly Asn Leu Thr Asn Leu Glu Arg Leu Tyr Leu
                395                 400                 405

Asn Arg Asn Lys Ile Glu Lys Ile Pro Thr Gln Leu Phe Tyr Cys
                410                 415                 420

Arg Lys Leu Arg Tyr Leu Asp Leu Ser His Asn Asn Leu Thr Phe
                425                 430                 435

Leu Pro Ala Asp Ile Gly Leu Leu Gln Asn Leu Gln Asn Leu Ala
                440                 445                 450

Ile Thr Ala Asn Arg Ile Glu Thr Leu Pro Pro Glu Leu Phe Gln
                455                 460                 465

Cys Arg Lys Leu Arg Ala Leu His Leu Gly Asn Asn Val Leu Gln
                470                 475                 480
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Ser Leu Pro Ser Arg Val Gly Glu Leu Thr Asn Leu Thr Gln Ile
485 490 495

Glu Leu Arg Gly Asn Arg Leu Glu Cys Leu Pro Val Glu Leu Gly
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Glu Cys Pro Leu Leu Lys Arg Ser Gly Leu Val Val Glu Glu Asp
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Leu Phe Asn Thr Leu Pro Pro Glu Val Lys Glu Arg Leu Trp Arg
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Ala Asp Lys Glu Gln Ala
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<211> 20
<212> DNA
<213> Artificial Sequence

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<223> Synthetic Oligonucleotide Probe

<400> 251
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<210> 254
<211> 1650
<212> DNA
<213> Homo Sapien

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ccaggctgcc agtctcctat ttgtggataa tcccgtgggc actgggttca 400

gttatgtgaa tggtagtggt gcctatgcca aggacctggc tatggtggct 450

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<210> 255
<211> 452
<212> PRT
<213> Homo Sapien

<400> 255

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Leu Leu Pro Leu Leu Leu Gly Leu Asn Ala Gly Ala Val Ile Asp
            20                  25                  30

Trp Pro Thr Glu Glu Gly Lys Glu Val Trp Asp Tyr Val Thr Val
            35                  40                  45

Arg Lys Asp Ala Tyr Met Phe Trp Trp Leu Tyr Tyr Ala Thr Asn
            50                  55                  60

Ser Cys Lys Asn Phe Ser Glu Leu Pro Leu Val Met Trp Leu Gln
            65                  70                  75

Gly Gly Pro Gly Gly Ser Ser Thr Gly Phe Gly Asn Phe Glu Glu
            80                  85                  90

Ile Gly Pro Leu Asp Ser Asp Leu Lys Pro Arg Lys Thr Thr Trp
            95                  100                 105

Leu Gln Ala Ala Ser Leu Leu Phe Val Asp Asn Pro Val Gly Thr
           110                 115                 120

Gly Phe Ser Tyr Val Asn Gly Ser Gly Ala Tyr Ala Lys Asp Leu
           125                 130                 135

Ala Met Val Ala Ser Asp Met Met Val Leu Leu Lys Thr Phe Phe
           140                 145                 150

Ser Cys His Lys Glu Phe Gln Thr Val Pro Phe Tyr Ile Phe Ser
           155                 160                 165

Glu Ser Tyr Gly Gly Lys Met Ala Ala Gly Ile Gly Leu Glu Leu
           170                 175                 180

Tyr Lys Ala Ile Gln Arg Gly Thr Ile Lys Cys Asn Phe Ala Gly
           185                 190                 195

Val Ala Leu Gly Asp Ser Trp Ile Ser Pro Val Asp Ser Val Leu
           200                 205                 210

Ser Trp Gly Pro Tyr Leu Tyr Ser Met Ser Leu Leu Glu Asp Lys
           215                 220                 225

Gly Leu Ala Glu Val Ser Lys Val Ala Glu Gln Val Leu Asn Ala
           230                 235                 240

Val Asn Lys Gly Leu Tyr Arg Glu Ala Thr Glu Leu Trp Gly Lys
           245                 250                 255

Ala Glu Met Ile Ile Glu Gln Asn Thr Asp Gly Val Asn Phe Tyr
           260                 265                 270

Asn Ile Leu Thr Lys Ser Thr Pro Thr Ser Thr Met Glu Ser Ser
           275                 280                 285

Leu Glu Phe Thr Gln Ser His Leu Val Cys Leu Cys Gln Arg His
           290                 295                 300

Val Arg His Leu Gln Arg Asp Ala Leu Ser Gln Leu Met Asn Gly
           305                 310                 315
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Pro Ile Arg Lys Lys Leu Lys Ile Ile Pro Glu Asp Gln Ser Trp
320 325 330

Gly Gly Gln Ala Thr Asn Val Phe Val Asn Met Glu Glu Asp Phe
335 340 345

Met Lys Pro Val Ile Ser Ile Val Asp Glu Leu Leu Glu Ala Gly
350 355 360

Ile Asn Val Thr Val Tyr Asn Gly Gln Leu Asp Leu Ile Val Asp
365 370 375

Thr Met Gly Gln Glu Ala Trp Val Arg Lys Leu Lys Trp Pro Glu
380 385 390

Leu Pro Lys Phe Ser Gln Leu Lys Trp Lys Ala Leu Tyr Ser Asp
395 400 405

Pro Lys Ser Leu Glu Thr Ser Ala Phe Val Lys Ser Tyr Lys Asn
410 415 420

Leu Ala Phe Tyr Trp Ile Leu Lys Ala Gly His Met Val Pro Ser
425 430 435

Asp Gln Gly Asp Met Ala Leu Lys Met Met Arg Leu Val Thr Gln
440 445 450

Gln Glu

<210> 256
<211> 1100
<212> DNA
<213> Homo Sapien

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<210> 257
<211> 314
<212> PRT
<213> Homo Sapien

<400> 257

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Ala	Gly	Leu	Arg	Lys	Pro	Glu	Ser	Gln	Glu	Ala	Ala	Pro	Leu	Ser
			20						25					30

Gly	Pro	Cys	Gly	Arg	Arg	Val	Ile	Thr	Ser	Arg	Ile	Val	Gly	Gly
			35						40					45

Glu	Asp	Ala	Glu	Leu	Gly	Arg	Trp	Pro	Trp	Gln	Gly	Ser	Leu	Arg
			50						55					60

Leu	Trp	Asp	Ser	His	Val	Cys	Gly	Val	Ser	Leu	Leu	Ser	His	Arg
			65						70					75

Trp	Ala	Leu	Thr	Ala	Ala	His	Cys	Phe	Glu	Thr	Tyr	Ser	Asp	Leu
			80						85					90

Ser	Asp	Pro	Ser	Gly	Trp	Met	Val	Gln	Phe	Gly	Gln	Leu	Thr	Ser
			95						100					105

Met	Pro	Ser	Phe	Trp	Ser	Leu	Gln	Ala	Tyr	Tyr	Thr	Arg	Tyr	Phe
			110						115					120

Val	Ser	Asn	Ile	Tyr	Leu	Ser	Pro	Arg	Tyr	Leu	Gly	Asn	Ser	Pro
			125						130					135

Tyr	Asp	Ile	Ala	Leu	Val	Lys	Leu	Ser	Ala	Pro	Val	Thr	Tyr	Thr
			140						145					150

Lys	His	Ile	Gln	Pro	Ile	Cys	Leu	Gln	Ala	Ser	Thr	Phe	Glu	Phe
			155						160					165

Glu	Asn	Arg	Thr	Asp	Cys	Trp	Val	Thr	Gly	Trp	Gly	Tyr	Ile	Lys
			170						175					180

Glu	Asp	Glu	Ala	Leu	Pro	Ser	Pro	His	Thr	Leu	Gln	Glu	Val	Gln
			185						190					195

Val Ala Ile Ile Asn Asn Ser Met Cys Asn His Leu Phe Leu Lys
200 205 210

Tyr Ser Phe Arg Lys Asp Ile Phe Gly Asp Met Val Cys Ala Gly
215 220 225

Asn Ala Gln Gly Gly Lys Asp Ala Cys Phe Gly Asp Ser Gly Gly
230 235 240

Pro Leu Ala Cys Asn Lys Asn Gly Leu Trp Tyr Gln Ile Gly Val
245 250 255

Val Ser Trp Gly Val Gly Cys Gly Arg Pro Asn Arg Pro Gly Val
260 265 270

Tyr Thr Asn Ile Ser His His Phe Glu Trp Ile Gln Lys Leu Met
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Ala Gln Ser Gly Met Ser Gln Pro Asp Pro Ser Trp Pro Leu Leu
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Phe Phe Pro Leu Leu Trp Ala Leu Pro Leu Leu Gly Pro Val
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<211> 2427
<212> DNA
<213> Homo Sapien

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tgtagatttt tgctcttctc agtttactca ttgtcccctg gaacaaatca 2350

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<210> 259
<211> 556
<212> PRT
<213> Homo Sapien

<400> 259

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             20                  25                  30

Leu Pro Pro Gly Trp Val Ser Leu Gly Arg Ala Asp Pro Glu Glu
             35                  40                  45

Glu Leu Ser Leu Thr Phe Ala Leu Arg Gln Gln Asn Val Glu Arg
             50                  55                  60

Leu Ser Glu Leu Val Gln Ala Val Ser Asp Pro Ser Ser Pro Gln
             65                  70                  75

Tyr Gly Lys Tyr Leu Thr Leu Glu Asn Val Ala Asp Leu Val Arg
             80                  85                  90

Pro Ser Pro Leu Thr Leu His Thr Val Gln Lys Trp Leu Leu Ala
             95                 100                 105

Ala Gly Ala Gln Lys Cys His Ser Val Ile Thr Gln Asp Phe Leu
            110                 115                 120

Thr Cys Trp Leu Ser Ile Arg Gln Ala Glu Leu Leu Leu Pro Gly
            125                 130                 135

Ala Glu Phe His His Tyr Val Gly Gly Pro Thr Glu Thr His Val
            140                 145                 150

Val Arg Ser Pro His Pro Tyr Gln Leu Pro Gln Ala Leu Ala Pro
            155                 160                 165

His Val Asp Phe Val Gly Gly Leu His Arg Phe Pro Pro Thr Ser
            170                 175                 180

Ser Leu Arg Gln Arg Pro Glu Pro Gln Val Thr Gly Thr Val Gly
            185                 190                 195

Leu His Leu Gly Val Thr Pro Ser Val Ile Arg Lys Arg Tyr Asn
            200                 205                 210

Leu Thr Ser Gln Asp Val Gly Ser Gly Thr Ser Asn Asn Ser Gln
            215                 220                 225

Ala Cys Ala Gln Phe Leu Glu Gln Tyr Phe His Asp Ser Asp Leu
            230                 235                 240

Ala Gln Phe Met Arg Leu Phe Gly Gly Asn Phe Ala His Gln Ala
            245                 250                 255

Ser Val Ala Arg Val Val Gly Gln Gln Gly Arg Gly Arg Ala Gly
            260                 265                 270

Ile Glu Ala Ser Leu Asp Val Gln Tyr Leu Met Ser Ala Gly Ala
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275 280 285

Asn Ile Ser Thr Trp Val Tyr Ser Ser Pro Gly Arg His Glu Gly
290 295 300

Gln Glu Pro Phe Leu Gln Trp Leu Met Leu Leu Ser Asn Glu Ser
305 310 315

Ala Leu Pro His Val His Thr Val Ser Tyr Gly Asp Asp Glu Asp
320 325 330

Ser Leu Ser Ser Ala Tyr Ile Gln Arg Val Asn Thr Glu Leu Met
335 340 345

Lys Ala Ala Ala Arg Gly Leu Thr Leu Leu Phe Ala Ser Gly Asp
350 355 360

Ser Gly Ala Gly Cys Trp Ser Val Ser Gly Arg His Gln Phe Arg
365 370 375

Pro Thr Phe Pro Ala Ser Ser Pro Tyr Val Thr Thr Val Gly Gly
380 385 390

Thr Ser Phe Gln Glu Pro Phe Leu Ile Thr Asn Glu Ile Val Asp
395 400 405

Tyr Ile Ser Gly Gly Gly Phe Ser Asn Val Phe Pro Arg Pro Ser
410 415 420

Tyr Gln Glu Glu Ala Val Thr Lys Phe Leu Ser Ser Ser Pro His
425 430 435

Leu Pro Pro Ser Ser Tyr Phe Asn Ala Ser Gly Arg Ala Tyr Pro
440 445 450

Asp Val Ala Ala Leu Ser Asp Gly Tyr Trp Val Val Ser Asn Arg
455 460 465

Val Pro Ile Pro Trp Val Ser Gly Thr Ser Ala Ser Thr Pro Val
470 475 480

Phe Gly Gly Ile Leu Ser Leu Ile Asn Glu His Arg Ile Leu Ser
485 490 495

Gly Arg Pro Pro Leu Gly Phe Leu Asn Pro Arg Leu Tyr Gln Gln
500 505 510

His Gly Ala Gly Leu Phe Asp Val Thr Arg Gly Cys His Glu Ser
515 520 525

Cys Leu Asp Glu Glu Val Glu Gly Gln Gly Phe Cys Ser Gly Pro
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Gly Trp Asp Pro Val Thr Gly Trp Gly Thr Pro Thr Ser Gln Leu
545 550 555

Cys

<210> 260
<211> 1638
<212> DNA
<213> Homo Sapien

<400> 260

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ttccctcctg gcagcaatta agggtcttca tgttcttatt ttaggagagg 1300

ccaaattgtt ttttgtcatt ggcgtgcaca cgtgtgtgtg tgtgtgtgtg 1350

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tgactggctt tactatttga aaactggttt gtgtatcata tcatatatca 1450

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tttggggcaa tgaggaatat ttgacaatta agttaatctt cacgtttttg 1550

caaactttga tttttatttc atctgaactt gtttcaaaga tttatattaa 1600

atatttggca tacaagagat atgaaaaaaa aaaaaaaa 1638

<210> 261
<211> 383
<212> PRT
<213> Homo Sapien

<400> 261

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				20				25						30	
Thr	Trp	Pro	Ala	Tyr	Arg	Leu	Pro	Val	Val	Leu	Pro	Gln	Ser	Thr	
				35				40						45	
Leu	Asn	Leu	Ala	Lys	Pro	Asp	Phe	Gly	Ala	Glu	Ala	Lys	Leu	Glu	
				50				55						60	
Val	Ser	Ser	Ser	Cys	Gly	Pro	Gln	Cys	His	Lys	Gly	Thr	Pro	Leu	
				65				70						75	
Pro	Thr	Tyr	Glu	Glu	Ala	Lys	Gln	Tyr	Leu	Ser	Tyr	Glu	Thr	Leu	
				80				85						90	
Tyr	Ala	Asn	Gly	Ser	Arg	Thr	Glu	Thr	Gln	Val	Gly	Ile	Tyr	Ile	
				95				100						105	
Leu	Ser	Ser	Ser	Gly	Asp	Gly	Ala	Gln	His	Arg	Asp	Ser	Gly	Ser	
				110				115						120	
Ser	Gly	Lys	Ser	Arg	Arg	Lys	Arg	Gln	Ile	Tyr	Gly	Tyr	Asp	Ser	
				125				130						135	
Arg	Phe	Ser	Ile	Phe	Gly	Lys	Asp	Phe	Leu	Leu	Asn	Tyr	Pro	Phe	
				140				145						150	
Ser	Thr	Ser	Val	Lys	Leu	Ser	Thr	Gly	Cys	Thr	Gly	Thr	Leu	Val	
				155				160						165	
Ala	Glu	Lys	His	Val	Leu	Thr	Ala	Ala	His	Cys	Ile	His	Asp	Gly	
				170				175						180	
Lys	Thr	Tyr	Val	Lys	Gly	Thr	Gln	Lys	Leu	Arg	Val	Gly	Phe	Leu	
				185				190						195	
Lys	Pro	Lys	Phe	Lys	Asp	Gly	Gly	Arg	Gly	Ala	Asn	Asp	Ser	Thr	
				200				205						210	
Ser	Ala	Met	Pro	Glu	Gln	Met	Lys	Phe	Gln	Trp	Ile	Arg	Val	Lys	
				215				220						225	
Arg	Thr	His	Val	Pro	Lys	Gly	Trp	Ile	Lys	Gly	Asn	Ala	Asn	Asp	
				230				235						240	
Ile	Gly	Met	Asp	Tyr	Asp	Tyr	Ala	Leu	Leu	Glu	Leu	Lys	Lys	Pro	
				245				250						255	
His	Lys	Arg	Lys	Phe	Met	Lys	Ile	Gly	Val	Ser	Pro	Pro	Ala	Lys	

260 265 270

Gln Leu Pro Gly Gly Arg Ile His Phe Ser Gly Tyr Asp Asn Asp
275 280 285

Arg Pro Gly Asn Leu Val Tyr Arg Phe Cys Asp Val Lys Asp Glu
290 295 300

Thr Tyr Asp Leu Leu Tyr Gln Gln Cys Asp Ala Gln Pro Gly Ala
305 310 315

Ser Gly Ser Gly Val Tyr Val Arg Met Trp Lys Arg Gln Gln Gln
320 325 330

Lys Trp Glu Arg Lys Ile Ile Gly Ile Phe Ser Gly His Gln Trp
335 340 345

Val Asp Met Asn Gly Ser Pro Gln Asp Phe Asn Val Ala Val Arg
350 355 360

Ile Thr Pro Leu Lys Tyr Ala Gln Ile Cys Tyr Trp Ile Lys Gly
365 370 375

Asn Tyr Leu Asp Cys Arg Glu Gly
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<210> 262
<211> 1378
<212> DNA
<213> Homo Sapien

<400> 262
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caggatacct gttcccccag cctgtgggaa gccccagcag ctgaaccggg 200

ttgtgggcgg cgaggacagc actgacagcg agtggccctg gatcgtgagc 250

atccagaaga atgggaccca ccactgcgca ggttctctgc tcaccagccg 300

ctgggtgatc actgctgccc actgtttcaa ggacaacctg aacaaaccat 350

acctgttctc tgtgctgctg ggggcctggc agctggggaa ccctggctct 400

cggtcccaga aggtgggtgt tgcctgggtg gagccccacc ctgtgtattc 450

ctggaaggaa ggtgcctgtg cagacattgc cctggtgcgt ctcgagcgct 500

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atccacctcc ctccaaacac ccactgctgg atctcaggct gggggagcat 600

ccaagatgga gttcccttgc cccaccctca gaccctgcag aagctgaagg 650

ttcctatcat cgactcggaa gtctgcagcc atctgtactg gcggggagca 700

ggacagggac ccatcactga ggacatgctg tgtgccggct acttggaggg 750

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cccgcccccg ggccccagcg cttttgtgta tataaatgtt aatgattttt 1300

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ataaattatt tattctccaa aaaaaaaa 1378

<210> 263
<211> 317
<212> PRT
<213> Homo Sapien

<400> 263

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Gly	Thr	Phe	Thr	Ser	Leu	Leu	Leu	Leu	Ala	Ser	Thr	Ala	Ile	Leu
				20				25					30	
Asn	Ala	Ala	Arg	Ile	Pro	Val	Pro	Pro	Ala	Cys	Gly	Lys	Pro	Gln
				35				40					45	
Gln	Leu	Asn	Arg	Val	Val	Gly	Gly	Glu	Asp	Ser	Thr	Asp	Ser	Glu
				50				55					60	
Trp	Pro	Trp	Ile	Val	Ser	Ile	Gln	Lys	Asn	Gly	Thr	His	His	Cys
				65				70					75	
Ala	Gly	Ser	Leu	Leu	Thr	Ser	Arg	Trp	Val	Ile	Thr	Ala	Ala	His
				80				85					90	
Cys	Phe	Lys	Asp	Asn	Leu	Asn	Lys	Pro	Tyr	Leu	Phe	Ser	Val	Leu
				95				100					105	
Leu	Gly	Ala	Trp	Gln	Leu	Gly	Asn	Pro	Gly	Ser	Arg	Ser	Gln	Lys
				110				115					120	
Val	Gly	Val	Ala	Trp	Val	Glu	Pro	His	Pro	Val	Tyr	Ser	Trp	Lys
				125				130					135	
Glu	Gly	Ala	Cys	Ala	Asp	Ile	Ala	Leu	Val	Arg	Leu	Glu	Arg	Ser
				140				145					150	
Ile	Gln	Phe	Ser	Glu	Arg	Val	Leu	Pro	Ile	Cys	Leu	Pro	Asp	Ala
				155				160					165	

Ser Ile His Leu Pro Pro Asn Thr His Cys Trp Ile Ser Gly Trp
170 175 180

Gly Ser Ile Gln Asp Gly Val Pro Leu Pro His Pro Gln Thr Leu
185 190 195

Gln Lys Leu Lys Val Pro Ile Ile Asp Ser Glu Val Cys Ser His
200 205 210

Leu Tyr Trp Arg Gly Ala Gly Gln Gly Pro Ile Thr Glu Asp Met
215 220 225

Leu Cys Ala Gly Tyr Leu Glu Gly Glu Arg Asp Ala Cys Leu Gly
230 235 240

Asp Ser Gly Gly Pro Leu Met Cys Gln Val Asp Gly Ala Trp Leu
245 250 255

Leu Ala Gly Ile Ile Ser Trp Gly Glu Gly Cys Ala Glu Arg Asn
260 265 270

Arg Pro Gly Val Tyr Ile Ser Leu Ser Ala His Arg Ser Trp Val
275 280 285

Glu Lys Ile Val Gln Gly Val Gln Leu Arg Gly Arg Ala Gln Gly
290 295 300

Gly Gly Ala Leu Arg Ala Pro Ser Gln Gly Ser Gly Ala Ala Ala
305 310 315

Arg Ser

<210> 264
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<213> Artificial Sequence

<220>
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<210> 265
<211> 19
<212> DNA
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<220>
<223> Synthetic Oligonucleotide Probe

<400> 265
gcagaggtgt ctaaggttg 19

<210> 266
<211> 24
<212> DNA
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<220>
<223> Synthetic Oligonucleotide Probe

<400> 266
agctctagac caatgccagc ttcc 24

<210> 267
<211> 45
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<210> 268
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<400> 268
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<210> 269
<211> 24
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<400> 269
gaatgccctg caagcatcaa ctgg 24

<210> 270
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<210> 271
<211> 26
<212> DNA
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<400> 271
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<210> 272
<211> 18
<212> DNA
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<223> Synthetic Oligonucleotide Probe

<400> 272
cagccctgcc acatgtgc 18

<210> 273
<211> 18
<212> DNA
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<223> Synthetic Oligonucleotide Probe

<400> 273
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<210> 274
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<220>
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<400> 274
ggcgaagagc agggtgagac cccg 24

<210> 275
<211> 45
<212> DNA
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<220>
<223> Synthetic Oligonucleotide Probe

<400> 275
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<400> 276
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<210> 277
<211> 18
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<400> 277
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<210> 278

<211> 18
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<210> 279
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<400> 279
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<210> 280
<211> 45
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<400> 280
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<210> 281
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
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<400> 281
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<210> 282
<211> 61
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 282
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tgccaggtgg a 61

<210> 283
<211> 119
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 283
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gcagccatct gtactggcgg ggagcaggac agggacccat cactgaggac 100

atgctgtgtg ccggctact 119

<210> 284
<211> 1875
<212> DNA
<213> Homo Sapien

<400> 284
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ccgctactgc tactgctggt ggccaccaca ggccccgttg gagccctcac 100

agatgaggag aaacgtttga tggtggagct gcacaacctc taccgggccc 150

aggtatcccc gacggcctca gacatgctgc acatgagatg ggacgaggag 200

ctggccgcct tcgccaaggc ctacgcacgg cagtgcgtgt ggggccacaa 250

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ggactgcaca ccgggcccac acctctcctg cccctccctc ctgagtcctg 1650

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tgcccacaca gcatgtgcgc tctccctgag tgcctgtgta gctggggatg 1750

gggattccta ggggcagatg aaggacaagc cccactggag tggggttctt 1800

tgagtggggg aggcagggac gagggaagga aagtaactcc tgactctcca 1850

ataaaaacct gtccaacctg tgaaa 1875

<210> 285
<211> 463
<212> PRT
<213> Homo Sapien

<400> 285

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Leu	Leu	Leu	Val	Ala	Thr	Thr	Gly	Pro	Val	Gly	Ala	Leu	Thr	Asp	
				20					25						30
Glu	Glu	Lys	Arg	Leu	Met	Val	Glu	Leu	His	Asn	Leu	Tyr	Arg	Ala	
				35					40						45
Gln	Val	Ser	Pro	Thr	Ala	Ser	Asp	Met	Leu	His	Met	Arg	Trp	Asp	
				50					55						60
Glu	Glu	Leu	Ala	Ala	Phe	Ala	Lys	Ala	Tyr	Ala	Arg	Gln	Cys	Val	
				65					70						75
Trp	Gly	His	Asn	Lys	Glu	Arg	Gly	Arg	Arg	Gly	Glu	Asn	Leu	Phe	
				80					85						90
Ala	Ile	Thr	Asp	Glu	Gly	Met	Asp	Val	Pro	Leu	Ala	Met	Glu	Glu	
				95					100						105
Trp	His	His	Glu	Arg	Glu	His	Tyr	Asn	Leu	Ser	Ala	Ala	Thr	Cys	
				110					115						120
Ser	Pro	Gly	Gln	Met	Cys	Gly	His	Tyr	Thr	Gln	Val	Val	Trp	Ala	
				125					130						135
Lys	Thr	Glu	Arg	Ile	Gly	Cys	Gly	Ser	His	Phe	Cys	Glu	Lys	Leu	
				140					145						150

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Gln Gly Val Glu Glu Thr Asn Ile Glu Leu Leu Val Cys Asn Tyr
                155                 160                 165

Glu Pro Pro Gly Asn Val Lys Gly Lys Arg Pro Tyr Gln Glu Gly
                170                 175                 180

Thr Pro Cys Ser Gln Cys Pro Ser Gly Tyr His Cys Lys Asn Ser
                185                 190                 195

Leu Cys Glu Pro Ile Gly Ser Pro Glu Asp Ala Gln Asp Leu Pro
                200                 205                 210

Tyr Leu Val Thr Glu Ala Pro Ser Phe Arg Ala Thr Glu Ala Ser
                215                 220                 225

Asp Ser Arg Lys Met Gly Thr Pro Ser Ser Leu Ala Thr Gly Ile
                230                 235                 240

Pro Ala Phe Leu Val Thr Glu Val Ser Gly Ser Leu Ala Thr Lys
                245                 250                 255

Ala Leu Pro Ala Val Glu Thr Gln Ala Pro Thr Ser Leu Ala Thr
                260                 265                 270

Lys Asp Pro Pro Ser Met Ala Thr Glu Ala Pro Pro Cys Val Thr
                275                 280                 285

Thr Glu Val Pro Ser Ile Leu Ala Ala His Ser Leu Pro Ser Leu
                290                 295                 300

Asp Glu Glu Pro Val Thr Phe Pro Lys Ser Thr His Val Pro Ile
                305                 310                 315

Pro Lys Ser Ala Asp Lys Val Thr Asp Lys Thr Lys Val Pro Ser
                320                 325                 330

Arg Ser Pro Glu Asn Ser Leu Asp Pro Lys Met Ser Leu Thr Gly
                335                 340                 345

Ala Arg Glu Leu Leu Pro His Ala Gln Glu Glu Ala Glu Ala Glu
                350                 355                 360

Ala Glu Leu Pro Pro Ser Ser Glu Val Leu Ala Ser Val Phe Pro
                365                 370                 375

Ala Gln Asp Lys Pro Gly Glu Leu Gln Ala Thr Leu Asp His Thr
                380                 385                 390

Gly His Thr Ser Ser Lys Ser Leu Pro Asn Phe Pro Asn Thr Ser
                395                 400                 405

Ala Thr Ala Asn Ala Thr Gly Gly Arg Ala Leu Ala Leu Gln Ser
                410                 415                 420

Ser Leu Pro Gly Ala Glu Gly Pro Asp Lys Pro Ser Val Val Ser
                425                 430                 435

Gly Leu Asn Ser Gly Pro Gly His Val Trp Gly Pro Leu Leu Gly
                440                 445                 450

Leu Leu Leu Leu Pro Pro Leu Val Leu Ala Gly Ile Phe
                455                 460
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<210> 286
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 286
tcctgcagtt tcctgatgc 19

<210> 287
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 287
ctcatattgc acaccagtaa ttcg 24

<210> 288
<211> 45
<212> DNA
<213> Artificial Sequence

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<223> Synthetic Oligonucleotide Probe

<400> 288
atgaggagaa acgtttgatg gtggagctgc acaacctcta ccggg 45

<210> 289
<211> 3662
<212> DNA
<213> Homo Sapien

<400> 289
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caaggcaagt tccatgagcc accttcaaag ccttcgagaa gtgaaactga 200

acaacaatga attggagacc attccaaatc tgggaccagt ctcggcaaat 250

attacacttc tctccttggc tggaaacagg attgttgaaa tactccctga 300

acatctgaaa gagtttcagt cccttgaaac tttggacctt agcagcaaca 350

atatttcaga gctccaaact gcatttccag ccctacagct caaatatctg 400

tatctcaaca gcaaccgagt cacatcaatg gaacctgggt attttgacaa 450

tttggccaac acactccttg tgttaaagct gaacaggaac cgaatctcag 500

ctatcccacc caagatgttt aaactgcccc aactgcaaca tctcgaattg 550

aaccgaaaca agattaaaaa tgtagatgga ctgacattcc aaggccttgg 600

tgctctgaag tctctgaaaa tgcaaagaaa tggagtaacg aaacttatgg 650

atggagcttt ttgggggctg agcaacatgg aaattttgca gctggaccat 700

aacaacctaa cagagattac caaaggctgg ctttacggct tgctgatgct 750

gcaggaactt catctcagcc aaaatgccat caacaggatc agccctgatg 800

cctgggagtt ctgccagaag ctcagtgagc tggacctaac tttcaatcac 850

ttatcaaggt tagatgattc aagcttcctt ggcctaagct tactaaatac 900

actgcacatt gggaacaaca gagtcagcta cattgctgat tgtgccttcc 950

gggggctttc cagtttaaag actttggatc tgaagaacaa tgaaatttcc 1000

tggactattg aagacatgaa tggtgctttc tctgggcttg acaaactgag 1050

gcgactgata ctccaaggaa atcggatccg ttctattact aaaaaagcct 1100

tcactggttt ggatgcattg gagcatctag acctgagtga caacgcaatc 1150

atgtctttac aaggcaatgc attttcacaa atgaagaaac tgcaacaatt 1200

gcatttaaat acatcaagcc ttttgtgcga ttgccagcta aaatggctcc 1250

cacagtgggt ggcggaaaac aactttcaga gctttgtaaa tgccagttgt 1300

gcccatcctc agctgctaaa aggaagaagc atttttgctg ttagcccaga 1350

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gccagcagca gtgattcccc aatgactttt gcttggaaaa aagacaatga 1500

actactgcat gatgctgaaa tggaaaatta tgcacacctc cgggcccaag 1550

gtggcgaggt gatggagtat accaccatcc ttcggctgcg cgaggtggaa 1600

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taaatcatga ttattttatg tatttttata atgccagatt tcttttttatg 3550

gaaaatgagt tactaaagca ttttaaataa tacctgcctt gtaccatttt 3600

ttaaatagaa gttacttcat tatattttgc acattatatt taataaaatg 3650

tgtcaatttg aa 3662

<210> 290
<211> 1059

<212> PRT
<213> Homo Sapien

<400> 290

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Met Val Asp Val Leu Leu Leu Phe Ser Leu Cys Leu Leu Phe His
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Ile Ser Arg Pro Asp Leu Ser His Asn Arg Leu Ser Phe Ile Lys
             20                  25                  30

Ala Ser Ser Met Ser His Leu Gln Ser Leu Arg Glu Val Lys Leu
             35                  40                  45

Asn Asn Asn Glu Leu Glu Thr Ile Pro Asn Leu Gly Pro Val Ser
             50                  55                  60

Ala Asn Ile Thr Leu Leu Ser Leu Ala Gly Asn Arg Ile Val Glu
             65                  70                  75

Ile Leu Pro Glu His Leu Lys Glu Phe Gln Ser Leu Glu Thr Leu
             80                  85                  90

Asp Leu Ser Ser Asn Asn Ile Ser Glu Leu Gln Thr Ala Phe Pro
             95                 100                 105

Ala Leu Gln Leu Lys Tyr Leu Tyr Leu Asn Ser Asn Arg Val Thr
            110                 115                 120

Ser Met Glu Pro Gly Tyr Phe Asp Asn Leu Ala Asn Thr Leu Leu
            125                 130                 135

Val Leu Lys Leu Asn Arg Asn Arg Ile Ser Ala Ile Pro Pro Lys
            140                 145                 150

Met Phe Lys Leu Pro Gln Leu Gln His Leu Glu Leu Asn Arg Asn
            155                 160                 165

Lys Ile Lys Asn Val Asp Gly Leu Thr Phe Gln Gly Leu Gly Ala
            170                 175                 180

Leu Lys Ser Leu Lys Met Gln Arg Asn Gly Val Thr Lys Leu Met
            185                 190                 195

Asp Gly Ala Phe Trp Gly Leu Ser Asn Met Glu Ile Leu Gln Leu
            200                 205                 210

Asp His Asn Asn Leu Thr Glu Ile Thr Lys Gly Trp Leu Tyr Gly
            215                 220                 225

Leu Leu Met Leu Gln Glu Leu His Leu Ser Gln Asn Ala Ile Asn
            230                 235                 240

Arg Ile Ser Pro Asp Ala Trp Glu Phe Cys Gln Lys Leu Ser Glu
            245                 250                 255

Leu Asp Leu Thr Phe Asn His Leu Ser Arg Leu Asp Asp Ser Ser
            260                 265                 270

Phe Leu Gly Leu Ser Leu Leu Asn Thr Leu His Ile Gly Asn Asn
            275                 280                 285

Arg Val Ser Tyr Ile Ala Asp Cys Ala Phe Arg Gly Leu Ser Ser
            290                 295                 300
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Leu Lys Thr Leu Asp Leu Lys Asn Asn Glu Ile Ser Trp Thr Ile
305 310 315

Glu Asp Met Asn Gly Ala Phe Ser Gly Leu Asp Lys Leu Arg Arg
320 325 330

Leu Ile Leu Gln Gly Asn Arg Ile Arg Ser Ile Thr Lys Lys Ala
335 340 345

Phe Thr Gly Leu Asp Ala Leu Glu His Leu Asp Leu Ser Asp Asn
350 355 360

Ala Ile Met Ser Leu Gln Gly Asn Ala Phe Ser Gln Met Lys Lys
365 370 375

Leu Gln Gln Leu His Leu Asn Thr Ser Ser Leu Leu Cys Asp Cys
380 385 390

Gln Leu Lys Trp Leu Pro Gln Trp Val Ala Glu Asn Asn Phe Gln
395 400 405

Ser Phe Val Asn Ala Ser Cys Ala His Pro Gln Leu Leu Lys Gly
410 415 420

Arg Ser Ile Phe Ala Val Ser Pro Asp Gly Phe Val Cys Asp Asp
425 430 435

Phe Pro Lys Pro Gln Ile Thr Val Gln Pro Glu Thr Gln Ser Ala
440 445 450

Ile Lys Gly Ser Asn Leu Ser Phe Ile Cys Ser Ala Ala Ser Ser
455 460 465

Ser Asp Ser Pro Met Thr Phe Ala Trp Lys Lys Asp Asn Glu Leu
470 475 480

Leu His Asp Ala Glu Met Glu Asn Tyr Ala His Leu Arg Ala Gln
485 490 495

Gly Gly Glu Val Met Glu Tyr Thr Thr Ile Leu Arg Leu Arg Glu
500 505 510

Val Glu Phe Ala Ser Glu Gly Lys Tyr Gln Cys Val Ile Ser Asn
515 520 525

His Phe Gly Ser Ser Tyr Ser Val Lys Ala Lys Leu Thr Val Asn
530 535 540

Met Leu Pro Ser Phe Thr Lys Thr Pro Met Asp Leu Thr Ile Arg
545 550 555

Ala Gly Ala Met Ala Arg Leu Glu Cys Ala Ala Val Gly His Pro
560 565 570

Ala Pro Gln Ile Ala Trp Gln Lys Asp Gly Gly Thr Asp Phe Pro
575 580 585

Ala Ala Arg Glu Arg Arg Met His Val Met Pro Glu Asp Asp Val
590 595 600

Phe Phe Ile Val Asp Val Lys Ile Glu Asp Ile Gly Val Tyr Ser
605 610 615

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Cys Thr Ala Gln Asn Ser Ala Gly Ser Ile Ser Ala Asn Ala Thr
620                 625                 630

Leu Thr Val Leu Glu Thr Pro Ser Phe Leu Arg Pro Leu Leu Asp
635                 640                 645

Arg Thr Val Thr Lys Gly Glu Thr Ala Val Leu Gln Cys Ile Ala
650                 655                 660

Gly Gly Ser Pro Pro Pro Lys Leu Asn Trp Thr Lys Asp Asp Ser
665                 670                 675

Pro Leu Val Val Thr Glu Arg His Phe Phe Ala Ala Gly Asn Gln
680                 685                 690

Leu Leu Ile Ile Val Asp Ser Asp Val Ser Asp Ala Gly Lys Tyr
695                 700                 705

Thr Cys Glu Met Ser Asn Thr Leu Gly Thr Glu Arg Gly Asn Val
710                 715                 720

Arg Leu Ser Val Ile Pro Thr Pro Thr Cys Asp Ser Pro Gln Met
725                 730                 735

Thr Ala Pro Ser Leu Asp Asp Asp Gly Trp Ala Thr Val Gly Val
740                 745                 750

Val Ile Ile Ala Val Val Cys Cys Val Val Gly Thr Ser Leu Val
755                 760                 765

Trp Val Val Ile Ile Tyr His Thr Arg Arg Arg Asn Glu Asp Cys
770                 775                 780

Ser Ile Thr Asn Thr Asp Glu Thr Asn Leu Pro Ala Asp Ile Pro
785                 790                 795

Ser Tyr Leu Ser Ser Gln Gly Thr Leu Ala Asp Arg Gln Asp Gly
800                 805                 810

Tyr Val Ser Ser Glu Ser Gly Ser His His Gln Phe Val Thr Ser
815                 820                 825

Ser Gly Ala Gly Phe Phe Leu Pro Gln His Asp Ser Ser Gly Thr
830                 835                 840

Cys His Ile Asp Asn Ser Ser Glu Ala Asp Val Glu Ala Ala Thr
845                 850                 855

Asp Leu Phe Leu Cys Pro Phe Leu Gly Ser Thr Gly Pro Met Tyr
860                 865                 870

Leu Lys Gly Asn Val Tyr Gly Ser Asp Pro Phe Glu Thr Tyr His
875                 880                 885

Thr Gly Cys Ser Pro Asp Pro Arg Thr Val Leu Met Asp His Tyr
890                 895                 900

Glu Pro Ser Tyr Ile Lys Lys Lys Glu Cys Tyr Pro Cys Ser His
905                 910                 915

Pro Ser Glu Glu Ser Cys Glu Arg Ser Phe Ser Asn Ile Ser Trp
920                 925                 930
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Pro Ser His Val Arg Lys Leu Leu Asn Thr Ser Tyr Ser His Asn
935 940 945

Glu Gly Pro Gly Met Lys Asn Leu Cys Leu Asn Lys Ser Ser Leu
950 955 960

Asp Phe Ser Ala Asn Pro Glu Pro Ala Ser Val Ala Ser Ser Asn
965 970 975

Ser Phe Met Gly Thr Phe Gly Lys Ala Leu Arg Arg Pro His Leu
980 985 990

Asp Ala Tyr Ser Ser Phe Gly Gln Pro Ser Asp Cys Gln Pro Arg
995 1000 1005

Ala Phe Tyr Leu Lys Ala His Ser Ser Pro Asp Leu Asp Ser Gly
1010 1015 1020

Ser Glu Glu Asp Gly Lys Glu Arg Thr Asp Phe Gln Glu Glu Asn
1025 1030 1035

His Ile Cys Thr Phe Lys Gln Thr Leu Glu Asn Tyr Arg Thr Pro
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Asn Phe Gln Ser Tyr Asp Leu Asp Thr
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<211> 2906
<212> DNA
<213> Homo Sapien

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tggaaccgaa cgcaatggat aaactgattg tgcaagagag aaggaagaac 150

gaagcttttt cttgtgagcc ctggatctta acacaaatgt gtatatgtgc 200

acacagggag cattcaagaa tgaaataaac cagagttaga cccgcggggg 250

ttggtgtgtt ctgacataaa taaataatct taaagcagct gttcccctcc 300

ccacccccaa aaaaaaggat gattggaaat gaagaaccga ggattcacaa 350

agaaaaaagt atgttcattt ttctctataa aggagaaagt gagccaagga 400

gatatttttg gaatgaaaag tttggggctt ttttagtaaa gtaaagaact 450

ggtgtggtgg tgttttcctt tctttttgaa tttcccacaa gaggagagga 500

aattaataat acatctgcaa agaaatttca gagaagaaaa gttgaccgcg 550

gcagattgag gcattgattg ggggagagaa accagcagag cacagttgga 600

tttgtgccta tgttgactaa aattgacgga taattgcagt tggatttttc 650

ttcatcaacc tccttttttt taaattttta ttccttttgg tatcaagatc 700

atgcgttttc tcttgttctt aaccacctgg atttccatct ggatgttgct 750

gtgatcagtc tgaaatacaa ctgtttgaat tccagaagga ccaacaccag 800

ataaattatg aatgttgaac aagatgacct tacatccaca gcagataatg 850

ataggtccta ggtttaacag ggccctattt gacccccctgc ttgtggtgct 900

gctggctctt caacttcttg tggtggctgg tctggtgcgg gctcagacct 950

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cggaaaaacc tgcgtgaggt tccggatggc atctccacca acacacggct 1050

gctgaacctc catgagaacc aaatccagat catcaaagtg aacagcttca 1100

agcacttgag gcacttggaa atcctacagt tgagtaggaa ccatatcaga 1150

accattgaaa ttggggcttt caatggtctg gcgaacctca acactctgga 1200

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tgtctaaact gaaggagctc tggttgcgaa acaaccccat tgaaagcatc 1300

ccttcttatg cttttaacag aattccttct ttgcgccgac tagacttagg 1350

ggaattgaaa agactttcat acatctcaga aggtgccttt gaaggtctgt 1400

ccaacttgag gtatttgaac cttgccatgt gcaaccttcg ggaaatccct 1450

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attactgcct catgacctct tcactccctt gcatcatcta gagcggatac 1700

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attacttcac atgctatgct ccggtgattg tggagccccc tgcagacctc 1900

aatgtcactg aaggcatggc agctgagctg aaatgtcggg cctccacatc 1950

cctgacatct gtatcttgga ttactccaaa tggaacagtc atgacacatg 2000

gggcgtacaa agtgcggata gctgtgctca gtgatggtac gttaaatttc 2050

acaaatgtaa ctgtgcaaga tacaggcatg tacacatgta tggtgagtaa 2100

ttccgttggg aatactactg cttcagccac cctgaatgtt actgcagcaa 2150

ccactactcc tttctcttac ttttcaaccg tcacagtaga gactatggaa 2200

ccgtctcagg atgaggcacg gaccacagat aacaatgtgg gtcccactcc 2250

agtggtcgac tgggagacca ccaatgtgac cacctctctc acaccacaga 2300

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tgactgggct aaatctactg tttcaaaaaa gtgtctttac aaaaaaacaa 2850

aaaagaaaag aaatttattt attaaaaatt ctattgtgat ctaaagcaga 2900

caaaaa 2906

<210> 292
<211> 640
<212> PRT
<213> Homo Sapien

<400> 292

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Pro	Arg	Phe	Asn	Arg	Ala	Leu	Phe	Asp	Pro	Leu	Leu	Val	Val	Leu
				20				25						30
Leu	Ala	Leu	Gln	Leu	Leu	Val	Val	Ala	Gly	Leu	Val	Arg	Ala	Gln
				35				40						45
Thr	Cys	Pro	Ser	Val	Cys	Ser	Cys	Ser	Asn	Gln	Phe	Ser	Lys	Val
				50				55						60
Ile	Cys	Val	Arg	Lys	Asn	Leu	Arg	Glu	Val	Pro	Asp	Gly	Ile	Ser
				65				70						75
Thr	Asn	Thr	Arg	Leu	Leu	Asn	Leu	His	Glu	Asn	Gln	Ile	Gln	Ile
				80				85						90
Ile	Lys	Val	Asn	Ser	Phe	Lys	His	Leu	Arg	His	Leu	Glu	Ile	Leu
				95				100						105
Gln	Leu	Ser	Arg	Asn	His	Ile	Arg	Thr	Ile	Glu	Ile	Gly	Ala	Phe
				110				115						120
Asn	Gly	Leu	Ala	Asn	Leu	Asn	Thr	Leu	Glu	Leu	Phe	Asp	Asn	Arg
				125				130						135
Leu	Thr	Thr	Ile	Pro	Asn	Gly	Ala	Phe	Val	Tyr	Leu	Ser	Lys	Leu
				140				145						150
Lys	Glu	Leu	Trp	Leu	Arg	Asn	Asn	Pro	Ile	Glu	Ser	Ile	Pro	Ser

155 160 165

Tyr Ala Phe Asn Arg Ile Pro Ser Leu Arg Arg Leu Asp Leu Gly
170 175 180

Glu Leu Lys Arg Leu Ser Tyr Ile Ser Glu Gly Ala Phe Glu Gly
185 190 195

Leu Ser Asn Leu Arg Tyr Leu Asn Leu Ala Met Cys Asn Leu Arg
200 205 210

Glu Ile Pro Asn Leu Thr Pro Leu Ile Lys Leu Asp Glu Leu Asp
215 220 225

Leu Ser Gly Asn His Leu Ser Ala Ile Arg Pro Gly Ser Phe Gln
230 235 240

Gly Leu Met His Leu Gln Lys Leu Trp Met Ile Gln Ser Gln Ile
245 250 255

Gln Val Ile Glu Arg Asn Ala Phe Asp Asn Leu Gln Ser Leu Val
260 265 270

Glu Ile Asn Leu Ala His Asn Asn Leu Thr Leu Leu Pro His Asp
275 280 285

Leu Phe Thr Pro Leu His His Leu Glu Arg Ile His Leu His His
290 295 300

Asn Pro Trp Asn Cys Asn Cys Asp Ile Leu Trp Leu Ser Trp Trp
305 310 315

Ile Lys Asp Met Ala Pro Ser Asn Thr Ala Cys Cys Ala Arg Cys
320 325 330

Asn Thr Pro Pro Asn Leu Lys Gly Arg Tyr Ile Gly Glu Leu Asp
335 340 345

Gln Asn Tyr Phe Thr Cys Tyr Ala Pro Val Ile Val Glu Pro Pro
350 355 360

Ala Asp Leu Asn Val Thr Glu Gly Met Ala Ala Glu Leu Lys Cys
365 370 375

Arg Ala Ser Thr Ser Leu Thr Ser Val Ser Trp Ile Thr Pro Asn
380 385 390

Gly Thr Val Met Thr His Gly Ala Tyr Lys Val Arg Ile Ala Val
395 400 405

Leu Ser Asp Gly Thr Leu Asn Phe Thr Asn Val Thr Val Gln Asp
410 415 420

Thr Gly Met Tyr Thr Cys Met Val Ser Asn Ser Val Gly Asn Thr
425 430 435

Thr Ala Ser Ala Thr Leu Asn Val Thr Ala Ala Thr Thr Thr Pro
440 445 450

Phe Ser Tyr Phe Ser Thr Val Thr Val Glu Thr Met Glu Pro Ser
455 460 465

Gln Asp Glu Ala Arg Thr Thr Asp Asn Asn Val Gly Pro Thr Pro

470 475 480

Val Val Asp Trp Glu Thr Thr Asn Val Thr Thr Ser Leu Thr Pro
485 490 495

Gln Ser Thr Arg Ser Thr Glu Lys Thr Phe Thr Ile Pro Val Thr
500 505 510

Asp Ile Asn Ser Gly Ile Pro Gly Ile Asp Glu Val Met Lys Thr
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Thr Lys Ile Ile Ile Gly Cys Phe Val Ala Ile Thr Leu Met Ala
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Ala Val Met Leu Val Ile Phe Tyr Lys Met Arg Lys Gln His His
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Arg Gln Asn His His Ala Pro Thr Arg Thr Val Glu Ile Ile Asn
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Val Asp Asp Glu Ile Thr Gly Asp Thr Pro Met Glu Ser His Leu
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Pro Met Pro Ala Ile Glu His Glu His Leu Asn His Tyr Asn Ser
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Tyr Lys Ser Pro Phe Asn His Thr Thr Thr Val Asn Thr Ile Asn
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Ser Lys Asp Asn Val Gln Glu Thr Gln Ile
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Gly Arg Gly Glu Leu Gly Gln Pro Ser Gly Val Ala Ala Glu Arg
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Pro Cys Pro Thr Thr Cys Arg Cys Leu Gly Asp Leu Leu Asp Cys
             50                  55                  60

Ser Arg Lys Arg Leu Ala Arg Leu Pro Glu Pro Leu Pro Ser Trp
             65                  70                  75

Val Ala Arg Leu Asp Leu Ser His Asn Arg Leu Ser Phe Ile Lys
             80                  85                  90

Ala Ser Ser Met Ser His Leu Gln Ser Leu Arg Glu Val Lys Leu
             95                 100                 105

Asn Asn Asn Glu Leu Glu Thr Ile Pro Asn Leu Gly Pro Val Ser
            110                 115                 120

Ala Asn Ile Thr Leu Leu Ser Leu Ala Gly Asn Arg Ile Val Glu
            125                 130                 135

Ile Leu Pro Glu His Leu Lys Glu Phe Gln Ser Leu Glu Thr Leu
            140                 145                 150

Asp Leu Ser Ser Asn Asn Ile Ser Glu Leu Gln Thr Ala Phe Pro
            155                 160                 165

Ala Leu Gln Leu Lys Tyr Leu Tyr Leu Asn Ser Asn Arg Val Thr
            170                 175                 180

Ser Met Glu Pro Gly Tyr Phe Asp Asn Leu Ala Asn Thr Leu Leu
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Val Leu Lys Leu Asn Arg Asn Arg Ile Ser Ala Ile Pro Pro Lys
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Met Phe Lys Leu Pro Gln Leu Gln His Leu Glu Leu Asn Arg Asn
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Lys Ile Lys Asn Val Asp Gly Leu Thr Phe Gln Gly Leu Gly Ala
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Leu Lys Ser Leu Lys Met Gln Arg Asn Gly Val Thr Lys Leu Met
                245                 250                 255

Asp Gly Ala Phe Trp Gly Leu Ser Asn Met Glu Ile Leu Gln Leu
                260                 265                 270

Asp His Asn Asn Leu Thr Glu Ile Thr Lys Gly Trp Leu Tyr Gly
                275                 280                 285

Leu Leu Met Leu Gln Glu Leu His Leu Ser Gln Asn Ala Ile Asn
                290                 295                 300

Arg Ile Ser Pro Asp Ala Trp Glu Phe Cys Gln Lys Leu Ser Glu
                305                 310                 315

Leu Asp Leu Thr Phe Asn His Leu Ser Arg Leu Asp Asp Ser Ser
                320                 325                 330

Phe Leu Gly Leu Ser Leu Leu Asn Thr Leu His Ile Gly Asn Asn
                335                 340                 345

Arg Val Ser Tyr Ile Ala Asp Cys Ala Phe Arg Gly Leu Ser Ser
                350                 355                 360

Leu Lys Thr Leu Asp Leu Lys Asn Asn Glu Ile Ser Trp Thr Ile
                365                 370                 375

Glu Asp Met Asn Gly Ala Phe Ser Gly Leu Asp Lys Leu Arg Arg
                380                 385                 390

Leu Ile Leu Gln Gly Asn Arg Ile Arg Ser Ile Thr Lys Lys Ala
                395                 400                 405

Phe Thr Gly Leu Asp Ala Leu Glu His Leu Asp Leu Ser Asp Asn
                410                 415                 420

Ala Ile Met Ser Leu Gln Gly Asn Ala Phe Ser Gln Met Lys Lys
                425                 430                 435

Leu Gln Gln Leu His Leu Asn Thr Ser Ser Leu Leu Cys Asp Cys
                440                 445                 450

Gln Leu Lys Trp Leu Pro Gln Trp Val Ala Glu Asn Asn Phe Gln
                455                 460                 465

Ser Phe Val Asn Ala Ser Cys Ala His Pro Gln Leu Leu Lys Gly
                470                 475                 480

Arg Ser Ile Phe Ala Val Ser Pro Asp Gly Phe Val Cys Asp Asp
                485                 490                 495

Phe Pro Lys Pro Gln Ile Thr Val Gln Pro Glu Thr Gln Ser Ala
                500                 505                 510

Ile Lys Gly Ser Asn Leu Ser Phe Ile Cys Ser Ala Ala Ser Ser
                515                 520                 525
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Ser Asp Ser Pro Met Thr Phe Ala Trp Lys Lys Asp Asn Glu Leu
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Leu His Asp Ala Glu Met Glu Asn Tyr Ala His Leu Arg Ala Gln
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Gly Gly Glu Val Met Glu Tyr Thr Thr Ile Leu Arg Leu Arg Glu
560                 565                 570

Val Glu Phe Ala Ser Glu Gly Lys Tyr Gln Cys Val Ile Ser Asn
575                 580                 585

His Phe Gly Ser Ser Tyr Ser Val Lys Ala Lys Leu Thr Val Asn
590                 595                 600

Met Leu Pro Ser Phe Thr Lys Thr Pro Met Asp Leu Thr Ile Arg
605                 610                 615

Ala Gly Ala Met Ala Arg Leu Glu Cys Ala Ala Val Gly His Pro
620                 625                 630

Ala Pro Gln Ile Ala Trp Gln Lys Asp Gly Gly Thr Asp Phe Pro
635                 640                 645

Ala Ala Arg Glu Arg Arg Met His Val Met Pro Glu Asp Asp Val
650                 655                 660

Phe Phe Ile Val Asp Val Lys Ile Glu Asp Ile Gly Val Tyr Ser
665                 670                 675

Cys Thr Ala Gln Asn Ser Ala Gly Ser Ile Ser Ala Asn Ala Thr
680                 685                 690

Leu Thr Val Leu Glu Thr Pro Ser Phe Leu Arg Pro Leu Leu Asp
695                 700                 705

Arg Thr Val Thr Lys Gly Glu Thr Ala Val Leu Gln Cys Ile Ala
710                 715                 720

Gly Gly Ser Pro Pro Pro Lys Leu Asn Trp Thr Lys Asp Asp Ser
725                 730                 735

Pro Leu Val Val Thr Glu Arg His Phe Phe Ala Ala Gly Asn Gln
740                 745                 750

Leu Leu Ile Ile Val Asp Ser Asp Val Ser Asp Ala Gly Lys Tyr
755                 760                 765

Thr Cys Glu Met Ser Asn Thr Leu Gly Thr Glu Arg Gly Asn Val
770                 775                 780

Arg Leu Ser Val Ile Pro Thr Pro Thr Cys Asp Ser Pro Gln Met
785                 790                 795

Thr Ala Pro Ser Leu Asp Asp Asp Gly Trp Ala Thr Val Gly Val
800                 805                 810

Val Ile Ile Ala Val Val Cys Cys Val Val Gly Thr Ser Leu Val
815                 820                 825

Trp Val Val Ile Ile Tyr His Thr Arg Arg Arg Asn Glu Asp Cys
830                 835                 840
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Ser Ile Thr Asn Thr Asp Glu Thr Asn Leu Pro Ala Asp Ile Pro
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Ser Tyr Leu Ser Ser Gln Gly Thr Leu Ala Asp Arg Gln Asp Gly
                860                 865                 870

Tyr Val Ser Ser Glu Ser Gly Ser His His Gln Phe Val Thr Ser
                875                 880                 885

Ser Gly Ala Gly Phe Phe Leu Pro Gln His Asp Ser Ser Gly Thr
                890                 895                 900

Cys His Ile Asp Asn Ser Ser Glu Ala Asp Val Glu Ala Ala Thr
                905                 910                 915

Asp Leu Phe Leu Cys Pro Phe Leu Gly Ser Thr Gly Pro Met Tyr
                920                 925                 930

Leu Lys Gly Asn Val Tyr Gly Ser Asp Pro Phe Glu Thr Tyr His
                935                 940                 945

Thr Gly Cys Ser Pro Asp Pro Arg Thr Val Leu Met Asp His Tyr
                950                 955                 960

Glu Pro Ser Tyr Ile Lys Lys Lys Glu Cys Tyr Pro Cys Ser His
                965                 970                 975

Pro Ser Glu Glu Ser Cys Glu Arg Ser Phe Ser Asn Ile Ser Trp
                980                 985                 990

Pro Ser His Val Arg Lys Leu Leu Asn Thr Ser Tyr Ser His Asn
                995                1000                1005

Glu Gly Pro Gly Met Lys Asn Leu Cys Leu Asn Lys Ser Ser Leu
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Asp Phe Ser Ala Asn Pro Glu Pro Ala Ser Val Ala Ser Ser Asn
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Ser Phe Met Gly Thr Phe Gly Lys Ala Leu Arg Arg Pro His Leu
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Asp Ala Tyr Ser Ser Phe Gly Gln Pro Ser Asp Cys Gln Pro Arg
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Ala Phe Tyr Leu Lys Ala His Ser Ser Pro Asp Leu Asp Ser Gly
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Ser Glu Glu Asp Gly Lys Glu Arg Thr Asp Phe Gln Glu Glu Asn
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<223> Synthetic Oligonucleotide Probe

<400> 313
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<210> 314
<211> 3003
<212> DNA
<213> Homo Sapien

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caacctgttc ctcgcgcgcc actgcgctgc gccccaggac ccgctgccca 200

acatggattt tctcctggcg ctggtgctgg tatcctcgct ctacctgcag 250

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tggcctatgt cgttatggtg ggaggattga ctgctgctgg ggctgggctc 350

gccagtcttg gggacagtgt cagcctgtgt gccaaccacg atgcaaacat 400

ggtgaatgta tcgggccaaa caagtgcaag tgtcatcctg gttatgctgg 450

aaaaacctgt aatcaagatc taaatgagtg tggcctgaag ccccggccct 500

gtaagcacag gtgcatgaac acttacggca gctacaagtg ctactgtctc 550

aacggatata tgctcatgcc ggatggttcc tgctcaagtg ccctgacctg 600

ctccatggca aactgtcagt atggctgtga tgttgttaaa ggacaaatac 650

ggtgccagtg cccatcccct ggcctgcacc tggctcctga tgggaggacc 700

tgtgtagatg ttgatgaatg tgctacagga agagcctcct gccctagatt 750

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caaccaccgg actgacaact atagcaccag ctgccagtac acctccagga 1300

gggattacag ttgacaacag ggtacagaca gaccctcaga aacccagagg 1350

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gtggatggat cagggagaaa gacaatgact tgcactggga accaatcagg 1450

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aat 3003

<210> 315
<211> 509
<212> PRT
<213> Homo Sapien

<400> 315

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				20					25						30
Ser	Ser	Ile	Gly	Leu	Cys	Arg	Tyr	Gly	Gly	Arg	Ile	Asp	Cys	Cys	
				35					40						45
Trp	Gly	Trp	Ala	Arg	Gln	Ser	Trp	Gly	Gln	Cys	Gln	Pro	Val	Cys	
				50					55						60
Gln	Pro	Arg	Cys	Lys	His	Gly	Glu	Cys	Ile	Gly	Pro	Asn	Lys	Cys	
				65					70						75
Lys	Cys	His	Pro	Gly	Tyr	Ala	Gly	Lys	Thr	Cys	Asn	Gln	Asp	Leu	
				80					85						90
Asn	Glu	Cys	Gly	Leu	Lys	Pro	Arg	Pro	Cys	Lys	His	Arg	Cys	Met	
				95					100						105
Asn	Thr	Tyr	Gly	Ser	Tyr	Lys	Cys	Tyr	Cys	Leu	Asn	Gly	Tyr	Met	
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Leu	Met	Pro	Asp	Gly	Ser	Cys	Ser	Ser	Ala	Leu	Thr	Cys	Ser	Met	
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Ala	Asn	Cys	Gln	Tyr	Gly	Cys	Asp	Val	Val	Lys	Gly	Gln	Ile	Arg	
				140					145						150
Cys	Gln	Cys	Pro	Ser	Pro	Gly	Leu	His	Leu	Ala	Pro	Asp	Gly	Arg	
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Thr	Cys	Val	Asp	Val	Asp	Glu	Cys	Ala	Thr	Gly	Arg	Ala	Ser	Cys	
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Pro	Arg	Phe	Arg	Gln	Cys	Val	Asn	Thr	Phe	Gly	Ser	Tyr	Ile	Cys	
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Gln Cys His Asp Ile Asp Glu Cys Ser Leu Gly Gln Tyr Gln Cys
                215                 220                 225

Ser Ser Phe Ala Arg Cys Tyr Asn Val Arg Gly Ser Tyr Lys Cys
                230                 235                 240

Lys Cys Lys Glu Gly Tyr Gln Gly Asp Gly Leu Thr Cys Val Tyr
                245                 250                 255

Ile Pro Lys Val Met Ile Glu Pro Ser Gly Pro Ile His Val Pro
                260                 265                 270

Lys Gly Asn Gly Thr Ile Leu Lys Gly Asp Thr Gly Asn Asn Asn
                275                 280                 285

Trp Ile Pro Asp Val Gly Ser Thr Trp Trp Pro Pro Lys Thr Pro
                290                 295                 300

Tyr Ile Pro Pro Ile Ile Thr Asn Arg Pro Thr Ser Lys Pro Thr
                305                 310                 315

Thr Arg Pro Thr Pro Lys Pro Thr Pro Ile Pro Thr Pro Pro Pro
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Pro Pro Pro Leu Pro Thr Glu Leu Arg Thr Pro Leu Pro Pro Thr
                335                 340                 345

Thr Pro Glu Arg Pro Thr Thr Gly Leu Thr Thr Ile Ala Pro Ala
                350                 355                 360

Ala Ser Thr Pro Pro Gly Gly Ile Thr Val Asp Asn Arg Val Gln
                365                 370                 375

Thr Asp Pro Gln Lys Pro Arg Gly Asp Val Phe Ser Val Leu Val
                380                 385                 390

His Ser Cys Asn Phe Asp His Gly Leu Cys Gly Trp Ile Arg Glu
                395                 400                 405

Lys Asp Asn Asp Leu His Trp Glu Pro Ile Arg Asp Pro Ala Gly
                410                 415                 420

Gly Gln Tyr Leu Thr Val Ser Ala Ala Lys Ala Pro Gly Gly Lys
                425                 430                 435

Ala Ala Arg Leu Val Leu Pro Leu Gly Arg Leu Met His Ser Gly
                440                 445                 450

Asp Leu Cys Leu Ser Phe Arg His Lys Val Thr Gly Leu His Ser
                455                 460                 465

Gly Thr Leu Gln Val Phe Val Arg Lys His Gly Ala His Gly Ala
                470                 475                 480

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Ile Thr Leu Arg Gly Ala Asp Ile Lys Ser Glu Ser Gln Arg
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<211> 24
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<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

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<210> 317
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 317
ttgcacttgt aggacccacg tacg 24

<210> 318
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

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<210> 319
<211> 2110
<212> DNA
<213> Homo Sapien

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caacaggtgc ttgctcgggg ctgaaggtga cagtgccatc acacactgtc 150

catggcgtca gaggtcaggc cctctaccta cccgtccact atggcttcca 200

cactccagca tcagacatcc agatcatatg gctatttgag agaccccaca 250

caatgcccaa atacttactg ggctctgtga ataagtctgt ggttcctgac 300

ttggaatacc aacacaagtt caccatgatg ccacccaatg catctctgct 350

tatcaaccca ctgcagttcc ctgatgaagg caattacatc gtgaaggtca 400

acattcaggg aaatggaact ctatctgcca gtcagaagat acaagtcacg 450

gttgatgatc ctgtcacaaa gccagtggtg cagattcatc ctccctctgg 500

ggctgtggag tatgtgggga acatgaccct gacatgccat gtggaagggg 550

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aaaaaaaaaa 2110

<210> 320

<211> 450
<212> PRT
<213> Homo Sapien

<400> 320

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Gly Val Arg Gly Gln Ala Leu Tyr Leu Pro Val His Tyr Gly Phe
             35                  40                  45

His Thr Pro Ala Ser Asp Ile Gln Ile Ile Trp Leu Phe Glu Arg
             50                  55                  60

Pro His Thr Met Pro Lys Tyr Leu Leu Gly Ser Val Asn Lys Ser
             65                  70                  75

Val Val Pro Asp Leu Glu Tyr Gln His Lys Phe Thr Met Met Pro
             80                  85                  90

Pro Asn Ala Ser Leu Leu Ile Asn Pro Leu Gln Phe Pro Asp Glu
             95                 100                 105

Gly Asn Tyr Ile Val Lys Val Asn Ile Gln Gly Asn Gly Thr Leu
            110                 115                 120

Ser Ala Ser Gln Lys Ile Gln Val Thr Val Asp Asp Pro Val Thr
            125                 130                 135

Lys Pro Val Val Gln Ile His Pro Pro Ser Gly Ala Val Glu Tyr
            140                 145                 150

Val Gly Asn Met Thr Leu Thr Cys His Val Glu Gly Gly Thr Arg
            155                 160                 165

Leu Ala Tyr Gln Trp Leu Lys Asn Gly Arg Pro Val His Thr Ser
            170                 175                 180

Ser Thr Tyr Ser Phe Ser Pro Gln Asn Asn Thr Leu His Ile Ala
            185                 190                 195

Pro Val Thr Lys Glu Asp Ile Gly Asn Tyr Ser Cys Leu Val Arg
            200                 205                 210

Asn Pro Val Ser Glu Met Glu Ser Asp Ile Ile Met Pro Ile Ile
            215                 220                 225

Tyr Tyr Gly Pro Tyr Gly Leu Gln Val Asn Ser Asp Lys Gly Leu
            230                 235                 240

Lys Val Gly Glu Val Phe Thr Val Asp Leu Gly Glu Ala Ile Leu
            245                 250                 255

Phe Asp Cys Ser Ala Asp Ser His Pro Pro Asn Thr Tyr Ser Trp
            260                 265                 270

Ile Arg Arg Thr Asp Asn Thr Thr Tyr Ile Ile Lys His Gly Pro
            275                 280                 285

Arg Leu Glu Val Ala Ser Glu Lys Val Ala Gln Lys Thr Met Asp
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290 295 300

Tyr Val Cys Cys Ala Tyr Asn Asn Ile Thr Gly Arg Gln Asp Glu
305 310 315

Thr His Phe Thr Val Ile Ile Thr Ser Val Gly Leu Glu Lys Leu
320 325 330

Ala Gln Lys Gly Lys Ser Leu Ser Pro Leu Ala Ser Ile Thr Gly
335 340 345

Ile Ser Leu Phe Leu Ile Ile Ser Met Cys Leu Leu Phe Leu Trp
350 355 360

Lys Lys Tyr Gln Pro Tyr Lys Val Ile Lys Gln Lys Leu Glu Gly
365 370 375

Arg Pro Glu Thr Glu Tyr Arg Lys Ala Gln Thr Phe Ser Gly His
380 385 390

Glu Asp Ala Leu Asp Asp Phe Gly Ile Tyr Glu Phe Val Ala Phe
395 400 405

Pro Asp Val Ser Gly Val Ser Arg Ile Pro Ser Arg Ser Val Pro
410 415 420

Ala Ser Asp Cys Val Ser Gly Gln Asp Leu His Ser Thr Val Tyr
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<223> Synthetic Oligonucleotide Probe

<400> 322
cactgacagg gttcctcacc cagg 24

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<211> 45
<212> DNA
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<220>
<223> Synthetic Oligonucleotide Probe

<400> 323

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<210> 324
<211> 2397
<212> DNA
<213> Homo Sapien

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aaacctttct aaccacttca ttaaagctga aaaaaaaaaa aaaaaaa 2397

<210> 325
<211> 280
<212> PRT
<213> Homo Sapien

<400> 325

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			20					25						30	
Val	Arg	Val	Ile	Thr	Asp	Glu	Asn	Trp	Arg	Glu	Leu	Leu	Glu	Gly
			35					40						45	
Asp	Trp	Met	Ile	Glu	Phe	Tyr	Ala	Pro	Trp	Cys	Pro	Ala	Cys	Gln
			50					55						60	
Asn	Leu	Gln	Pro	Glu	Trp	Glu	Ser	Phe	Ala	Glu	Trp	Gly	Glu	Asp
			65					70						75	
Leu	Glu	Val	Asn	Ile	Ala	Lys	Val	Asp	Val	Thr	Glu	Gln	Pro	Gly

80 85 90

Leu Ser Gly Arg Phe Ile Ile Thr Ala Leu Pro Thr Ile Tyr His
95 100 105

Cys Lys Asp Gly Glu Phe Arg Arg Tyr Gln Gly Pro Arg Thr Lys
110 115 120

Lys Asp Phe Ile Asn Phe Ile Ser Asp Lys Glu Trp Lys Ser Ile
125 130 135

Glu Pro Val Ser Ser Trp Phe Gly Pro Gly Ser Val Leu Met Ser
140 145 150

Ser Met Ser Ala Leu Phe Gln Leu Ser Met Trp Ile Arg Thr Cys
155 160 165

His Asn Tyr Phe Ile Glu Asp Leu Gly Leu Pro Val Trp Gly Ser
170 175 180

Tyr Thr Val Phe Ala Leu Ala Thr Leu Phe Ser Gly Leu Leu Leu
185 190 195

Gly Leu Cys Met Ile Phe Val Ala Asp Cys Leu Cys Pro Ser Lys
200 205 210

Arg Arg Arg Pro Gln Pro Tyr Pro Tyr Pro Ser Lys Lys Leu Leu
215 220 225

Ser Glu Ser Ala Gln Pro Leu Lys Lys Val Glu Glu Glu Gln Glu
230 235 240

Ala Asp Glu Glu Asp Val Ser Glu Glu Glu Ala Glu Ser Lys Glu
245 250 255

Gly Thr Asn Lys Asp Phe Pro Gln Asn Ala Ile Arg Gln Arg Ser
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Leu Gly Pro Ser Leu Ala Thr Asp Lys Ser
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<210> 326
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<213> Artificial Sequence

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<400> 327
tatgtggatc aggacgtgcc 20

<210> 328
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<212> DNA
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<210> 329
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<212> DNA
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<400> 329
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<210> 330
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<210> 331
<211> 2168
<212> DNA
<213> Homo Sapien

<400> 331
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ggacaggcgg attggaagag cgggaaggtc ctggcccaga gcagtgtgac 150

acttccctct gtgaccatga aactctgggt gtctgcattg ctgatggcct 200

ggtttggtgt cctgagctgt gtgcaggccg aattcttcac ctctattggg 250

cacatgactg acctgattta tgcagagaaa gagctggtgc agtctctgaa 300

agagtacatc cttgtggagg aagccaagct ttccaagatt aagagctggg 350

ccaacaaaat ggaagccttg actagcaagt cagctgctga tgctgagggc 400

tacctggctc accctgtgaa tgcctacaaa ctggtgaagc ggctaaacac 450

agactggcct gcgctggagg accttgtcct gcaggactca gctgcaggtt 500

ttatcgccaa cctctctgtg cagcggcagt tcttccccac tgatgaggac 550

gagataggag ctgccaaagc cctgatgaga cttcaggaca catacaggct 600

ggacccaggc acaatttcca gaggggaact tccaggaacc aagtaccagg 650

caatgctgag tgtggatgac tgctttggga tgggccgctc ggcctacaat 700

gaaggggact attatcatac ggtgttgtgg atggagcagg tgctaaagca 750

gcttgatgcc ggggaggagg ccaccacaac caagtcacag gtgctggact 800

acctcagcta tgctgtcttc cagttgggtg atctgcaccg tgccctggag 850

ctcacccgcc gcctgctctc ccttgaccca agccacgaac gagctggagg 900

gaatctgcgg tactttgagc agttattgga ggaagagaga gaaaaaacgt 950

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ggtaccacca tggcaacagg gccccacagc tgctcattgc ccccttcaaa 1150

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cacgagccac cgttcgtgat cccaagacag gagtcctcac tgtcgccagc 1300

taccgggttt ccaaaagctc ctggctagag gaagatgatg accctgttgt 1350

ggcccgagta aatcgtcgga tgcagcatat cacagggtta acagtaaaga 1400

ctgcagaatt gttacaggtt gcaaattatg gagtgggagg acagtatgaa 1450

ccgcacttcg acttctctag gcgacctttt gacagcggcc tcaaaacaga 1500

ggggaatagg ttagcgacgt ttcttaacta catgagtgat gtagaagctg 1550

gtggtgccac cgtcttccct gatctggggg ctgcaatttg gcctaagaag 1600

ggtacagctg tgttctggta caacctcttg cggagcgggg aaggtgacta 1650

ccgaacaaga catgctgcct gccctgtgct tgtgggctgc aagtgggtct 1700

ccaataagtg gttccatgaa cgaggacagg agttcttgag accttgtgga 1750

tcaacagaag ttgactgaca tccttttctg tccttccccc tcctggtcct 1800

tcagcccatg tcaacgtgac agacaccttt gtatgttcct ttgtatgttc 1850

ctatcaggct gatttttgga gaaatgaatg tttgtctgga gcagagggag 1900

accatactag ggcgactcct gtgtgactga agtcccagcc cttccattca 1950

gcctgtgcca tccctggccc caaggctagg atcaaagtgg ctgcagcaga 2000

gttagctgtc tagcgcctag caaggtgcct ttgtacctca ggtgttttag 2050

gtgtgagatg tttcagtgaa ccaaagttct gataccttgt ttacatgttt 2100

gtttttatgg catttctatc tattgtggct ttaccaaaaa ataaaatgtc 2150

cctaccagaa aaaaaaaa 2168

<210> 332
<211> 533
<212> PRT
<213> Homo Sapien

<400> 332

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Met Lys Leu Trp Val Ser Ala Leu Leu Met Ala Trp Phe Gly Val
  1               5                  10                  15

Leu Ser Cys Val Gln Ala Glu Phe Phe Thr Ser Ile Gly His Met
             20                  25                  30

Thr Asp Leu Ile Tyr Ala Glu Lys Glu Leu Val Gln Ser Leu Lys
             35                  40                  45

Glu Tyr Ile Leu Val Glu Glu Ala Lys Leu Ser Lys Ile Lys Ser
             50                  55                  60

Trp Ala Asn Lys Met Glu Ala Leu Thr Ser Lys Ser Ala Ala Asp
             65                  70                  75

Ala Glu Gly Tyr Leu Ala His Pro Val Asn Ala Tyr Lys Leu Val
             80                  85                  90

Lys Arg Leu Asn Thr Asp Trp Pro Ala Leu Glu Asp Leu Val Leu
             95                 100                 105

Gln Asp Ser Ala Ala Gly Phe Ile Ala Asn Leu Ser Val Gln Arg
            110                 115                 120

Gln Phe Phe Pro Thr Asp Glu Asp Glu Ile Gly Ala Ala Lys Ala
            125                 130                 135

Leu Met Arg Leu Gln Asp Thr Tyr Arg Leu Asp Pro Gly Thr Ile
            140                 145                 150

Ser Arg Gly Glu Leu Pro Gly Thr Lys Tyr Gln Ala Met Leu Ser
            155                 160                 165

Val Asp Asp Cys Phe Gly Met Gly Arg Ser Ala Tyr Asn Glu Gly
            170                 175                 180

Asp Tyr Tyr His Thr Val Leu Trp Met Glu Gln Val Leu Lys Gln
            185                 190                 195

Leu Asp Ala Gly Glu Glu Ala Thr Thr Thr Lys Ser Gln Val Leu
            200                 205                 210

Asp Tyr Leu Ser Tyr Ala Val Phe Gln Leu Gly Asp Leu His Arg
            215                 220                 225

Ala Leu Glu Leu Thr Arg Arg Leu Leu Ser Leu Asp Pro Ser His
            230                 235                 240

Glu Arg Ala Gly Gly Asn Leu Arg Tyr Phe Glu Gln Leu Leu Glu
            245                 250                 255

Glu Glu Arg Glu Lys Thr Leu Thr Asn Gln Thr Glu Ala Glu Leu
            260                 265                 270

Ala Thr Pro Glu Gly Ile Tyr Glu Arg Pro Val Asp Tyr Leu Pro
            275                 280                 285
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Glu Arg Asp Val Tyr Glu Ser Leu Cys Arg Gly Glu Gly Val Lys
290 295 300

Leu Thr Pro Arg Arg Gln Lys Arg Leu Phe Cys Arg Tyr His His
305 310 315

Gly Asn Arg Ala Pro Gln Leu Leu Ile Ala Pro Phe Lys Glu Glu
320 325 330

Asp Glu Trp Asp Ser Pro His Ile Val Arg Tyr Tyr Asp Val Met
335 340 345

Ser Asp Glu Glu Ile Glu Arg Ile Lys Glu Ile Ala Lys Pro Lys
350 355 360

Leu Ala Arg Ala Thr Val Arg Asp Pro Lys Thr Gly Val Leu Thr
365 370 375

Val Ala Ser Tyr Arg Val Ser Lys Ser Ser Trp Leu Glu Glu Asp
380 385 390

Asp Asp Pro Val Val Ala Arg Val Asn Arg Arg Met Gln His Ile
395 400 405

Thr Gly Leu Thr Val Lys Thr Ala Glu Leu Leu Gln Val Ala Asn
410 415 420

Tyr Gly Val Gly Gly Gln Tyr Glu Pro His Phe Asp Phe Ser Arg
425 430 435

Arg Pro Phe Asp Ser Gly Leu Lys Thr Glu Gly Asn Arg Leu Ala
440 445 450

Thr Phe Leu Asn Tyr Met Ser Asp Val Glu Ala Gly Gly Ala Thr
455 460 465

Val Phe Pro Asp Leu Gly Ala Ala Ile Trp Pro Lys Lys Gly Thr
470 475 480

Ala Val Phe Trp Tyr Asn Leu Leu Arg Ser Gly Glu Gly Asp Tyr
485 490 495

Arg Thr Arg His Ala Ala Cys Pro Val Leu Val Gly Cys Lys Trp
500 505 510

Val Ser Asn Lys Trp Phe His Glu Arg Gly Gln Glu Phe Leu Arg
515 520 525

Pro Cys Gly Ser Thr Glu Val Asp
530

<210> 333
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 333
ccaggcacaa tttccaga 18

<210> 334
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 334
ggacccttct gtgtgccag 19

<210> 335
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 335
ggtctcaaga actcctgtc 19

<210> 336
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 336
acactcagca ttgcctggta cttg 24

<210> 337
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<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 337
gggcacatga ctgacctgat ttatgcagag aaagagctgg tgcag 45

<210> 338
<211> 2789
<212> DNA
<213> Homo Sapien

<400> 338
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tcccagtgtg agtgaaattg attgtttcat ttattaccgt tttggctggg 100

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agacaggaca atcttcttgg ggatgctggt cctggaagcc agcgggcctt 200

gctctgtctt tggcctcatt gaccccaggt tctctggtta aaactgaaag 250

cctactactg gcctggtgcc catcaatcca ttgatccttg aggctgtgcc 300

cctggggcac ccacctggca gggcctacca ccatgcgact gagctccctg 350

ttggctctgc tgcggccagc gcttcccctc atcttagggc tgtctctggg 400

gtgcagcctg agcctcctgc gggtttcctg gatccagggg gagggagaag 450

atccctgtgt cgaggctgta ggggagcgag gagggccaca gaatccagat 500

tcgagagctc ggctagacca aagtgatgaa gacttcaaac cccggattgt 550

cccctactac agggacccca acaagcccta caagaaggtg ctcaggactc 600

ggtacatcca gacagagctg ggctcccgtg agcggttgct ggtggctgtc 650

ctgacctccc gagctacact gtccactttg gccgtggctg tgaaccgtac 700

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accctgagaa ggaagggagc tcggctttcc tgagtgcctt cgccgtgcac 1250

cctgtctccg aaggtaccct catgtaccgg ctccacaaac gcttcagcgc 1300

tctggagttg gagcgggctt acagtgaaat agaacaactg caggctcaga 1350

tccggaacct gaccgtgctg acccccgaag gggaggcagg gctgagctgg 1400

cccgttgggc tccctgctcc tttcacacca cactctcgct ttgaggtgct 1450

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ccaggaaggg caaggcaaga tggtggacag atagagaatt gttgctgtat 2750

tttttaaata tgaaaatgtt attaaacatg tcttctgcc 2789

<210> 339
<211> 772
<212> PRT
<213> Homo Sapien

<400> 339

Met	Arg	Leu	Ser	Ser	Leu	Leu	Ala	Leu	Leu	Arg	Pro	Ala	Leu	Pro
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Leu	Ile	Leu	Gly	Leu	Ser	Leu	Gly	Cys	Ser	Leu	Ser	Leu	Leu	Arg
			20					25					30	

Val	Ser	Trp	Ile	Gln	Gly	Glu	Gly	Glu	Asp	Pro	Cys	Val	Glu	Ala
			35					40					45	

Val	Gly	Glu	Arg	Gly	Gly	Pro	Gln	Asn	Pro	Asp	Ser	Arg	Ala	Arg
			50					55					60	

Leu	Asp	Gln	Ser	Asp	Glu	Asp	Phe	Lys	Pro	Arg	Ile	Val	Pro	Tyr
			65					70					75	

Tyr	Arg	Asp	Pro	Asn	Lys	Pro	Tyr	Lys	Lys	Val	Leu	Arg	Thr	Arg
			80					85					90	

Tyr	Ile	Gln	Thr	Glu	Leu	Gly	Ser	Arg	Glu	Arg	Leu	Leu	Val	Ala
			95					100					105	

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Val Leu Thr Ser Arg Ala Thr Leu Ser Thr Leu Ala Val Ala Val
                110                 115                 120

Asn Arg Thr Val Ala His His Phe Pro Arg Leu Leu Tyr Phe Thr
                125                 130                 135

Gly Gln Arg Gly Ala Arg Ala Pro Ala Gly Met Gln Val Val Ser
                140                 145                 150

His Gly Asp Glu Arg Pro Ala Trp Leu Met Ser Glu Thr Leu Arg
                155                 160                 165

His Leu His Thr His Phe Gly Ala Asp Tyr Asp Trp Phe Phe Ile
                170                 175                 180

Met Gln Asp Asp Thr Tyr Val Gln Ala Pro Arg Leu Ala Ala Leu
                185                 190                 195

Ala Gly His Leu Ser Ile Asn Gln Asp Leu Tyr Leu Gly Arg Ala
                200                 205                 210

Glu Glu Phe Ile Gly Ala Gly Glu Gln Ala Arg Tyr Cys His Gly
                215                 220                 225

Gly Phe Gly Tyr Leu Leu Ser Arg Ser Leu Leu Leu Arg Leu Arg
                230                 235                 240

Pro His Leu Asp Gly Cys Arg Gly Asp Ile Leu Ser Ala Arg Pro
                245                 250                 255

Asp Glu Trp Leu Gly Arg Cys Leu Ile Asp Ser Leu Gly Val Gly
                260                 265                 270

Cys Val Ser Gln His Gln Gly Gln Gln Tyr Arg Ser Phe Glu Leu
                275                 280                 285

Ala Lys Asn Arg Asp Pro Glu Lys Glu Gly Ser Ser Ala Phe Leu
                290                 295                 300

Ser Ala Phe Ala Val His Pro Val Ser Glu Gly Thr Leu Met Tyr
                305                 310                 315

Arg Leu His Lys Arg Phe Ser Ala Leu Glu Leu Glu Arg Ala Tyr
                320                 325                 330

Ser Glu Ile Glu Gln Leu Gln Ala Gln Ile Arg Asn Leu Thr Val
                335                 340                 345

Leu Thr Pro Glu Gly Glu Ala Gly Leu Ser Trp Pro Val Gly Leu
                350                 355                 360

Pro Ala Pro Phe Thr Pro His Ser Arg Phe Glu Val Leu Gly Trp
                365                 370                 375

Asp Tyr Phe Thr Glu Gln His Thr Phe Ser Cys Ala Asp Gly Ala
                380                 385                 390

Pro Lys Cys Pro Leu Gln Gly Ala Ser Arg Ala Asp Val Gly Asp
                395                 400                 405

Ala Leu Glu Thr Ala Leu Glu Gln Leu Asn Arg Arg Tyr Gln Pro
                410                 415                 420
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Arg Leu Arg Phe Gln Lys Gln Arg Leu Leu Asn Gly Tyr Arg Arg
425                 430                 435

Phe Asp Pro Ala Arg Gly Met Glu Tyr Thr Leu Asp Leu Leu Leu
440                 445                 450

Glu Cys Val Thr Gln Arg Gly His Arg Arg Ala Leu Ala Arg Arg
455                 460                 465

Val Ser Leu Leu Arg Pro Leu Ser Arg Val Glu Ile Leu Pro Met
470                 475                 480

Pro Tyr Val Thr Glu Ala Thr Arg Val Gln Leu Val Leu Pro Leu
485                 490                 495

Leu Val Ala Glu Ala Ala Ala Ala Pro Ala Phe Leu Glu Ala Phe
500                 505                 510

Ala Ala Asn Val Leu Glu Pro Arg Glu His Ala Leu Leu Thr Leu
515                 520                 525

Leu Leu Val Tyr Gly Pro Arg Glu Gly Gly Arg Gly Ala Pro Asp
530                 535                 540

Pro Phe Leu Gly Val Lys Ala Ala Ala Ala Glu Leu Glu Arg Arg
545                 550                 555

Tyr Pro Gly Thr Arg Leu Ala Trp Leu Ala Val Arg Ala Glu Ala
560                 565                 570

Pro Ser Gln Val Arg Leu Met Asp Val Val Ser Lys Lys His Pro
575                 580                 585

Val Asp Thr Leu Phe Phe Leu Thr Thr Val Trp Thr Arg Pro Gly
590                 595                 600

Pro Glu Val Leu Asn Arg Cys Arg Met Asn Ala Ile Ser Gly Trp
605                 610                 615

Gln Ala Phe Phe Pro Val His Phe Gln Glu Phe Asn Pro Ala Leu
620                 625                 630

Ser Pro Gln Arg Ser Pro Pro Gly Pro Pro Gly Ala Gly Pro Asp
635                 640                 645

Pro Pro Ser Pro Pro Gly Ala Asp Pro Ser Arg Gly Ala Pro Ile
650                 655                 660

Gly Gly Arg Phe Asp Arg Gln Ala Ser Ala Glu Gly Cys Phe Tyr
665                 670                 675

Asn Ala Asp Tyr Leu Ala Ala Arg Ala Arg Leu Ala Gly Glu Leu
680                 685                 690

Ala Gly Gln Glu Glu Glu Glu Ala Leu Glu Gly Leu Glu Val Met
695                 700                 705

Asp Val Phe Leu Arg Phe Ser Gly Leu His Leu Phe Arg Ala Val
710                 715                 720

Glu Pro Gly Leu Val Gln Lys Phe Ser Leu Arg Asp Cys Ser Pro
725                 730                 735
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Arg Leu Ser Glu Glu Leu Tyr His Arg Cys Arg Leu Ser Asn Leu
740 745 750

Glu Gly Leu Gly Gly Arg Ala Gln Leu Ala Met Ala Leu Phe Glu
755 760 765

Gln Glu Gln Ala Asn Ser Thr
770

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<211> 1572
<212> DNA
<213> Homo Sapien

<400> 340
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ctttttgaag ggtgtgatgc ttggaagcat tttctgtgct ttgatcacta 150

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catcatcacc tacaagctcc taacaaagaa gatatcttga aaatttcaga 250

ggatgagcgc atggagctca gtaagagctt tcgagtatac tgtattatcc 300

ttgtaaaacc caaagatgtg agtctttggg ctgcagtaaa ggagacttgg 350

accaaacact gtgacaaagc agagttcttc agttctgaaa atgttaaagt 400

gtttgagtca attaatatgg acacaaatga catgtggtta atgatgagaa 450

aagcttacaa atacgccttt gataagtata gagaccaata caactggttc 500

ttccttgcac gccccactac gtttgctatc attgaaaacc taaagtattt 550

tttgttaaaa aaggatccat cacagccttt ctatctaggc cacactataa 600

aatctggaga ccttgaatat gtgggtatgg aaggaggaat tgtcttaagt 650

gtagaatcaa tgaaaagact taacagcctt ctcaatatcc cagaaaagtg 700

tcctgaacag ggagggatga tttggaagat atctgaagat aaacagctag 750

cagtttgcct gaaatatgct ggagtatttg cagaaaatgc agaagatgct 800

gatggaaaag atgtatttaa taccaaatct gttgggcttt ctattaaaga 850

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gcaaatgata tctctagttg tgaatttgtg attaaagtaa aacttttagc 1450

tgtgtgttcc ctttacttct aatactgatt tatgttctaa gcctccccaa 1500

gttccaatgg atttgccttc tcaaaatgta caactaagca actaaagaaa 1550

attaaagtga aagttgaaaa at 1572

<210> 341
<211> 318
<212> PRT
<213> Homo Sapien

<400> 341

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Ser	Ile	Phe	Cys	Ala	Leu	Ile	Thr	Met	Leu	Gly	His	Ile	Arg	Ile
			20					25						30
Gly	His	Gly	Asn	Arg	Met	His	His	His	Glu	His	His	His	Leu	Gln
			35					40						45
Ala	Pro	Asn	Lys	Glu	Asp	Ile	Leu	Lys	Ile	Ser	Glu	Asp	Glu	Arg
			50					55						60
Met	Glu	Leu	Ser	Lys	Ser	Phe	Arg	Val	Tyr	Cys	Ile	Ile	Leu	Val
			65					70						75
Lys	Pro	Lys	Asp	Val	Ser	Leu	Trp	Ala	Ala	Val	Lys	Glu	Thr	Trp
			80					85						90
Thr	Lys	His	Cys	Asp	Lys	Ala	Glu	Phe	Phe	Ser	Ser	Glu	Asn	Val
			95					100						105
Lys	Val	Phe	Glu	Ser	Ile	Asn	Met	Asp	Thr	Asn	Asp	Met	Trp	Leu
			110					115						120
Met	Met	Arg	Lys	Ala	Tyr	Lys	Tyr	Ala	Phe	Asp	Lys	Tyr	Arg	Asp
			125					130						135
Gln	Tyr	Asn	Trp	Phe	Phe	Leu	Ala	Arg	Pro	Thr	Thr	Phe	Ala	Ile
			140					145						150
Ile	Glu	Asn	Leu	Lys	Tyr	Phe	Leu	Leu	Lys	Lys	Asp	Pro	Ser	Gln
			155					160						165
Pro	Phe	Tyr	Leu	Gly	His	Thr	Ile	Lys	Ser	Gly	Asp	Leu	Glu	Tyr
			170					175						180
Val	Gly	Met	Glu	Gly	Gly	Ile	Val	Leu	Ser	Val	Glu	Ser	Met	Lys
			185					190						195
Arg	Leu	Asn	Ser	Leu	Leu	Asn	Ile	Pro	Glu	Lys	Cys	Pro	Glu	Gln
			200					205						210

Gly Gly Met Ile Trp Lys Ile Ser Glu Asp Lys Gln Leu Ala Val
215 220 225

Cys Leu Lys Tyr Ala Gly Val Phe Ala Glu Asn Ala Glu Asp Ala
230 235 240

Asp Gly Lys Asp Val Phe Asn Thr Lys Ser Val Gly Leu Ser Ile
245 250 255

Lys Glu Ala Met Thr Tyr His Pro Asn Gln Val Val Glu Gly Cys
260 265 270

Cys Ser Asp Met Ala Val Thr Phe Asn Gly Leu Thr Pro Asn Gln
275 280 285

Met His Val Met Met Tyr Gly Val Tyr Arg Leu Arg Ala Phe Gly
290 295 300

His Ile Phe Asn Asp Ala Leu Val Phe Leu Pro Pro Asn Gly Ser
305 310 315

Asp Asn Asp

<210> 342
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 342
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<210> 343
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<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 343
ctggttcttc cttgcacg 18

<210> 344
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 344
gcccaaatgc cctaaggcgg tatacccc 28

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Phe Arg Ile Phe Gln Thr Cys Asp Glu Lys Lys Phe Gln Leu Pro
             50                  55                  60

Glu Asn Phe Thr Glu Leu Ser Cys Tyr Asn Tyr Gly Ser Gly Ser
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Val Lys Asn Cys Cys Pro Leu Asn Trp Glu Tyr Phe Gln Ser Ser
             80                  85                  90

Cys Tyr Phe Phe Ser Thr Asp Thr Ile Ser Trp Ala Leu Ser Leu
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Lys Asn Cys Ser Ala Met Gly Ala His Leu Val Val Ile Asn Ser
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Thr Met Arg Asp Ser Ser Asn Pro Arg Gln Asn Trp Asn Asp Val
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35 40 45

Phe Glu Ser Val Glu Leu Ser Cys Ile Ile Thr Asp Ser Gln Thr
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Ser Asp Pro Arg Ile Glu Trp Lys Lys Ile Gln Asp Glu Gln Thr
65 70 75

Thr Tyr Val Phe Phe Asp Asn Lys Ile Gln Gly Asp Leu Ala Gly
80 85 90

Arg Ala Glu Ile Leu Gly Lys Thr Ser Leu Lys Ile Trp Asn Val
95 100 105

Thr Arg Arg Asp Ser Ala Leu Tyr Arg Cys Glu Val Val Ala Arg
110 115 120

Asn Asp Arg Lys Glu Ile Asp Glu Ile Val Ile Glu Leu Thr Val
125 130 135

Gln Val Lys Pro Val Thr Pro Val Cys Arg Val Pro Lys Ala Val
140 145 150

Pro Val Gly Lys Met Ala Thr Leu His Cys Gln Glu Ser Glu Gly
155 160 165

His Pro Arg Pro His Tyr Ser Trp Tyr Arg Asn Asp Val Pro Leu
170 175 180

Pro Thr Asp Ser Arg Ala Asn Pro Arg Phe Arg Asn Ser Ser Phe
185 190 195

His Leu Asn Ser Glu Thr Gly Thr Leu Val Phe Thr Ala Val His
200 205 210

Lys Asp Asp Ser Gly Gln Tyr Tyr Cys Ile Ala Ser Asn Asp Ala
215 220 225

Gly Ser Ala Arg Cys Glu Glu Gln Glu Met Glu Val Tyr Asp Leu
230 235 240

Asn Ile Gly Gly Ile Ile Gly Gly Val Leu Val Val Leu Ala Val
245 250 255

Leu Ala Leu Ile Thr Leu Gly Ile Cys Cys Ala Tyr Arg Arg Gly
260 265 270

Tyr Phe Ile Asn Asn Lys Gln Asp Gly Glu Ser Tyr Lys Asn Pro
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Asp Phe Arg His Lys Ser Ser Phe Val Ile

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Cys Xaa Asn